Attorney's Docket No.: GNVPN.031USA

TRANSMITTAL LETTER TO THE U.S. ELECTED OFFICE (EO/US) - ENTRY INTO NATIONAL STAGE UNDER 35 USC 371

PCT/US99/25694	2 November 1999	5 November 1998
International Application No.	International Filing Date	Priority Date Claimed

ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME
Title of Invention

James M. Wilson and Weidong Xiao
Applicant(s) for EO/US

Box PCT
Assistant Commissioner for Patents
Washington, DC 20231
Attn: EO/US

Sir:

Applicant herewith submits to the United States Elected Office (EO/US) the following items under 35 USC 371:

(1) This express request to immediately begin national examination procedures (35 USC 371(f)).

(2) A copy of the cover sheet for the published International Application along with a copy of the specification as filed: 109 pages, including 5 pages of claims, 13 sheets of drawings, 59 pages of Sequence Listing, and a copy of the 4 pages International Search Report.

(3) a copy of the 5 page Request form.

(4) a first Preliminary Amendment for entry prior to calculation of the filing fees.

(5) our check in the amount of $1,420.00, covering the basic national fee as set forth in 37 CFR 1.492(a)(5) and based on the first Preliminary Amendment (16 total claims; 10 independent; and no multiple dependent).

(6) A Second Preliminary Amendment.

Express Mail No. ET033648243US

(7) Our check in the amount of $90.00, covering the extra claim fees after entry of the second Preliminary Amendment (25 total claims; 10 independent; and no multiple dependent).

(8) Two (2) pages partially-executed Combined Declaration and Power of Attorney form by first inventor.

(9) A 59 pages Sequence Listing (provided in specification).

(10) A 3.5" computer-readable diskette.

(11) A 1 page Statement under 37 CFR §1.821(f) and §1.825(a) and (b).

Copies of the following miscellaneous items are also enclosed:

(12) Copy of the 3 page Demand for International Preliminary Examination.

(13) Copy of the 10 page Written Opinion.

(14) Copy of the 11 page International Preliminary Examination Report.

The Combined Declaration and Power of Attorney form of the second inventor will be filed by the appropriate deadline under 37 CFR §1.495(c)(2) with the surcharge under 37 CFR §1.492(e).

Please charge any additional fees which may be required to effect entry into the National Phase and credit any overpayment to Deposit Account No. 08-3040.

Please direct all communications concerning this application to the undersigned.

Respectfully submitted,
HOWSON AND HOWSON
Attorneys for the Applicants

By _____

Cathy A. Rodroff
Registration No. 33,980
Spring House Corporate Center
Box 457
Spring House, PA 19477
Telephone: (215) 540-9210
Telefacsimile: (215) 540-5818

GNVPN.031USA

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of	)	Group Art Unit:
	)	
James M. Wilson et al	)	Examiner:
	)	
Appln. No. 09/807,802	)	
	)	
Filed: April 17, 2001	)	
	)	
For: ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME	)	February 20, 2002

Commissioner for Patents
Box Sequence
Washington, DC 20231

STATEMENT PURSUANT TO 37 CFR §1.825(a)&(b)

Sir:

A substitute Sequence Listing and a computer readable form of the substitute Sequence Listing are provided herewith. This Sequence Listing contains updated background information and is in PatentIn Version 3.1. No substantive changes have been made. The substitute Sequence Listing and computer readable copy contain no new matter.

This affirms that to the best of my knowledge and belief the content of the pages of the substitute Sequence Listing and this computer readable copy of said pages of the substitute Sequence Listing provided herewith are the same.

Respectfully submitted,

HOWSON AND HOWSON
Attorneys for the Applicants

By Cathy A Kodroff

Cathy A. Kodroff
Registration No. 33,980
Spring House Corporate Center
P.O. Box 457
Spring House, PA 19477
(215) 540-9206

GNVPN.031USA

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of	) Group Art Unit:
James M. Wilson et al	) Examiner:
Appln. No.	)
Filed: Herewith	)
For: ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME	) April 17, 2001

Assistant Commissioner for Patents
Washington, DC 20231

PRELIMINARY AMENDMENT

Sir:

Please amend the application as set forth below.

In the Claims

Cancel claims 7, 8, 12, 13, 15, 21 and 22 without prejudice.

REMARKS

After entry of this preliminary amendment, the pending claims are claims 1-6, 9-11, 14, 16-20, and 23. Claims 7, 8, 12, 13, 15, 21 and 22 are cancelled. No new matter is introduced by this preliminary amendment.

Express Mail No. EL033648243US

Applicants respectfully request that this preliminary amendment be entered prior to calculating the filing fees.

The Director of the U. S. Patent and Trademark Office is hereby authorized to charge any deficiency in any fees due with the filing of this paper or credit any overpayment in any fees to Deposit Account No. 08-3040.

Respectfully submitted,

HOWSON AND HOWSON
Attorneys for Applicant

By Cathy A Kodroff

Cathy A. Kodroff
Registration No. 33,980
Spring House Corporate Center
Box 457
Spring House, PA 19477
Telephone: (215) 540-9200
Telefacsimile: (215) 540-5818

GNVPN.031USA

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of	) Group Art Unit:
James M. Wilson et al	) Examiner:
Appln. No.	)
Filed: Herewith	)
For: ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME	) April 17, 2001

Assistant Commissioner for Patents
Washington, DC 20231

SECOND PRELIMINARY AMENDMENT

Sir:

Please amend the application as follows.

In the Specification

Page 1, line 6, before "Field of the Invention", insert the following new paragraph:

-- Cross-Reference to Related Applications

This is a 371 of PCT/US99/25694, which claims the benefit of the priority of US Patent Application No. 60/107,114, filed November 5, 1998. --

Please enter the attached Abstract of the Disclosure on the attached page as new page 38.

Express Mail No ET033648243US

In the Claims

Add new claims 24-32 as follows.

24. The recombinant vector according to claim 3, wherein said vector further comprises AAV-1 capsid proteins having the sequence of SEQ ID NO: 13, 15 or 17 or functional fragments thereof.

25. The recombinant vector according to claim 3, wherein said vector further comprises adenovirus sequences.

26. The host cell transduced with a recombinant viral vector according to claim 3.

27. The host cell transduced with a nucleic acid molecule according to claim 1.

28. The host cell transduced with a nucleic acid molecule according to claim 2.

29. The host cell transduced with a nucleic acid molecule according to claim 10.

30. The host cell transduced with a nucleic acid molecule according to claim 11.

31. The pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 3.

32. The method for delivery of a transgene comprising the step of delivering to a host cell a recombinant virus comprising a recombinant vector according to claim 3.

REMARKS

Upon entry of this preliminary amendment, the claims pending are claims 1-6, 9-11, 14, 16-20, and 23-32. New claims 24-32 are supported throughout the specification and additionally by now cancelled original claims 7, 8, 12, 13, 15, and 22, respectively. New claims 24-32 have been added to incorporate the subject matter of canceled claims 7, 8, 12, 13, 15, and 22, as well as to correct dependencies. No new matter is introduced by this preliminary amendment. A clean copy of all of the pending claims is attached as Appendix A.

The attached Abstract of the Disclosure is supported throughout the specification.

Applicants respectfully request consideration of the amended pending claims.

The Director of the U. S. Patent and Trademark Office is hereby authorized to charge any deficiency in any fees due with the filing of this paper or credit any overpayment in any fees paid on the filing, or during prosecution of this application to Deposit Account No. 08-3040.

Respectfully submitted,

HOWSON AND HOWSON
Attorneys for Applicant

By _____
Cathy A. Kodroff
Registration No. 33,980
Spring House Corporate Center
Box 457
Spring House, PA 19477
Telephone: (215) 540-9200
Telefacsimile: (215) 540-5818

APPENDIX A - PENDING CLAIMS

1. An isolated AAV-1 nucleic acid molecule comprising a sequence selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) a DNA sequence complementary to SEQ ID NO: 1;

(c) cDNA complementary to (a) or (b); and

(d) RNA complementary to any of (a) to (c).

2. A nucleic acid molecule comprising an AAV-1 inverted terminal repeat (ITR) sequence selected from the group consisting of:

(a) nt 1 to 143 of SEQ ID NO: 1;

(b) nt 4576 to 4718 of SEQ ID NO: 1;

(c) a nucleic acid sequence complementary to (a) or (b); and

(d) a functional fragment of (a), (b), or (c).

3. A recombinant vector comprising a 5' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:

(a) nt 1 to 143 of SEQ ID NO: 1;

(b) a nucleic acid sequence complementary to (a); and

(c) a functional fragment of (a) or (b).

4. The recombinant vector according to claim 3, wherein said vector further comprises a 3' AAV-1 ITR.

5. A recombinant vector comprising a 3' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:

(a) nt 4576 to 4718 of SEQ ID NO: 1;

(b) a nucleic acid sequence complementary to (a); and

(c) a functional fragment of (a) or (b).

6. The recombinant vector according to claim 5, wherein said vector further comprises a 5' AAV-1 ITR.

9. A recombinant vector comprising an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1 or a functional fragment thereof.

10. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said cap coding region comprises at least one member is selected from the group consisting of:

(a) vp1, nt 2223 to 4431 of SEQ ID NO: 1;

(b) vp2, nt 2634 to 4432 of SEQ ID NO: 1; and

(c) vp3, nt 2829 to 4432 of SEQ ID NO: 1.

11. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said rep coding region comprises an AAV-1 rep coding region comprising at least one member selected from the group consisting of:

(a) rep 78, nt 335 to 2304 of SEQ ID NO: 1;

(b) rep 68, nt 335 to 2272 of SEQ ID NO: 1 or the c DNA corresponding thereto;

(c) rep 52, nt 1007 to 2304 of SEQ ID NO: 1; and

(d) rep 40, nt 1007 to 2272 of SEQ ID NO: 1 or the cDNA corresponding thereto.

14. A host cell stably transduced with an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1.

16. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 7.

17. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 8.

18. A method for AAV-mediated delivery of a transgene comprising the step of delivering to a host cell an AAV virion which comprises:

(a) a capsid comprising at least one capsid protein encoded by an AAV-1 cap gene; and

(b) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

19. A method for AAV-mediated delivery of a transgene to a host comprising the steps of:

(a) assaying a sample from the host to determine the presence of neutralizing antibodies specific against any serotype of AAV; and

(b) delivering to the host an AAV virion which comprises:

(i) a capsid comprising at least one capsid protein encoded by a cap gene of an AAV serotype against which the host has no antibodies as determined in step (a); and

(ii) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

20. The method according to claim 19, comprising the additional step of repeating steps (a) and (b).

23. A method for producing a selected gene product comprising the steps of transfecting a mammalian cell with the molecule according to claim 1 or a functional fragment thereof and culturing said cell under conditions suitable to express said gene product.

24. The recombinant vector according to claim 3, wherein said vector further comprises AAV-1 capsid proteins having the sequence of SEQ ID NO: 13, 15 or 17 or functional fragments thereof.

25. The recombinant vector according to claim 3, wherein said vector further comprises adenovirus sequences.

26. The host cell transduced with a recombinant viral vector according to claim 3.

27. The host cell transduced with a nucleic acid molecule according to claim 1.

28. The host cell transduced with a nucleic acid molecule according to claim 2.

29. The host cell transduced with a nucleic acid molecule according to claim 10.

30. The host cell transduced with a nucleic acid molecule according to claim 11.

31. The pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 3.

32. The method for delivery of a transgene comprising the step of delivering to a host cell a recombinant virus comprising a recombinant vector according to claim 3.

ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME

This work was supported by the National Institutes of Health, grant no. P30 DK47757-06 and PO1 HD32649-04. The US government may have certain rights in this invention.

Field of the Invention

This invention relates generally to viral vector, and more particularly, to recombinant viral vectors useful for gene delivery.

Background of the Invention

Adeno-associated viruses are small, single-stranded DNA viruses which require helper virus to facilitate efficient replication [K.I. Berns, *Parvoviridae: the viruses and their replication,* p. 1007-1041, in F.N. Fields et al., Fundamental virology, 3rd ed., vol. 2, (Lippencott-Raven Publishers, Philadelphia, PA) (1995)]. The 4.7 kb genome of AAV is characterized by two inverted terminal repeats (ITR) and two open reading frames which encode the Rep proteins and Cap proteins, respectively. The Rep reading frame encodes four proteins of molecular weight 78 kD, 68 kD, 52 kD and 40 kD. These proteins function mainly in regulating AAV replication and integration of the AAV into a host cell's chromosomes. The Cap reading frame encodes three structural proteins in molecular weight 85 kD (VP 1), 72 kD (VP2) and 61 kD (VP3) [Berns, cited above]. More than 80% of total proteins in AAV virion comprise VP3. The two ITRs are the only cis elements essential for AAV replication, packaging and integration. There are two conformations of AAV ITRs called "flip" and "flop". These differences in conformation originated from the replication model of adeno-associated virus which use the ITR to initiate and reinitiate the replication [R.O. Snyder et al., J. Virol., 67:6096-6104 (1993); K.I. Berns, Microbiological Reviews, 54:316-329 (1990)].

AAVs have been found in many animal species, including primates, canine, fowl and human [F.A. Murphy et al., "The Classification and Nomenclature of Viruses: Sixth Report of the International Committee on Taxonomy of Viruses",

Archives of Virology, (Springer-Verlag, Vienna) (1995)]. In addition to five known primate AAVs (AAV-1 to AAV-5), AAV-6, another serotype closely related to AAV-2 and AAV-1 has also been isolated [E. A. Rutledge et al., J. Virol., 72:309-319 (1998)]. Among all known AAV serotypes, AAV-2 is perhaps the most well-characterized serotype, because its infectious clone was the first made [R.J. Samulski et al., Proc. Natl, Acad. Sci USA, 79:2077-2081 (1982)]. Subsequently, the full sequences for AAV-3A, AAV-3B, AAV-4 and AAV-6 have also been determined [Rutledge, cited above; J.A.Chiorini et al., J. Virol., 71:6823-6833 (1997); S. Muramatsu et al., Virol., 221:208-217 (1996)]. Generally, all AAVs share more than 80% homology in nucleotide sequence.

A number of unique properties make AAV a promising vector for human gene therapy [Muzyczka, Current Topics in Microbiology and Immunology, 158:97-129 (1992)]. Unlike other viral vectors, AAVs have not been shown to be associated with any known human disease and are generally not considered pathogenic. Wild type AAV is capable of integrating into host chromosomes in a site specific manner [R. M. Kotin et al., Proc, Natl. Acad, Sci, USA, 87:2211-2215 (1990)- R.J. Samulski, EMBO J., 10(12):3941-3950 (1991)]. Recombinant AAV vectors can integrate into tissue cultured cells in chromosome 19 if the rep proteins are supplied in *trans* [C. Balague et al., J. Virol., 71:3299-3306 (1997); R. T. Surosky et al., J Virol., 71:7951-7959 (1997)]. The integrated genomes of AAV have been shown to allow long term gene expression in a number of tissues, including, muscle, liver, and brain [K. J. Fisher, Nature Med., 3(3):306-312 (1997); R. 0. Snyder et al., Nature Genetics, 16:270-276 (1997); X. Xiao et al., Experimental Neurology, 144:113-124 (1997); Xiao, J. Virol., 70(11):8098-8108 (1996)].

AAV-2 has been shown to be present in about 80-90% of the human population. Earlier studies showed that neutralizing antibodies for AAV-2 are prevalent [W. P. Parks et al., J. Virol., 2:716-722 (1970)]. The presence of such antibodies may significantly decrease the usefulness of AAV vectors based on AAV-2 despite its other merits. What are needed in the art are vectors characterized by the

advantages of AAV-2, including those described above, without the disadvantages, including the presence of neutralizing antibodies.

Summary of the Invention

In one aspect, the invention provides an isolated AAV-1 nucleic acid molecule which is selected from among SEQ ID NO: 1, the strand complementary to SEQ ID NO: 1, and cDNA and RNA sequences complementary to SEQ ID NO: 1 and its complementary strand.

In another aspect, the present invention provides AAV ITR sequences, which include the 5' ITR sequences, nt 1 to 143 of SEQ ID NO. 1; the 3' ITR sequences, nt 4576 to 4718 of SEQ ID NO: 1, and fragments thereof.

In yet another aspect, the present invention provides a recombinant vector comprising an AAV-1 ITR and a selected transgene. Preferably, the vector comprises both the 5' and 3' AAV-1 ITRs between which the selected transgene is located.

In still another aspect, the invention provides a recombinant vector comprising an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1 or a functional fragment thereof.

In a further aspect, the present invention provides a nucleic acid molecule encoding an AAV-1 rep coding region and an AAV-1 cap coding region.

In still another aspect, the present invention provides a host cell transduced with a recombinant viral vector of the invention. The invention further provides a host cell stably transduced with an AAV-1 P5 promoter of the invention.

In still a further aspect, the present invention provides a pharmaceutical composition comprising a carrier and a vector of the invention.

In yet another aspect, the present invention provides a method for AAV--mediated delivery of a transgene to a host involving the step of delivering to a selected host a recombinant viral vector comprising a selected transgene under the control of sequences which direct expression thereof and an adeno-associated virus 1 (AAV-1) virion.

In another aspect, the invention provides a method for in vitro production of a selected gene product using a vector of the invention.

Other aspects and advantages of the invention will be readily apparent to one of skill in the art from the detailed description of the invention.

Brief Description of the Drawings

Figs 1A-1C illustrate the alignment of nucleotides of AAV-1 [SEQ ID NO: 1], AAV-2 [SEQ ID NO. 18] and AAV-6 [SEQ ID NO: 19]. The alignment was done with MacVector 6.0. The full sequences of AAV-1 are shown in the top line. Nucleotides in AAV-2 and AAV-6 identical to AAV-1 are symbolized by "." and gaps by "-". Some of the conserved features among AAVs are marked in this figure. Note the 3' ITRs of AAV-1 and AAV-6 are shown in different orientations.

Fig. 2 illustrates the predicted secondary structure of AAV-1 ITR. The nucleotides in AAV-2 and AAV-6 are shown in italic and bold respectively.

Fig. 3A illustrates a hypothesis of how AAV-6 arose from the homologous recombination between AAV-1 and AAV-2. The major elements of AAV-1 are indicated in the graph. A region that is shared between AAV-1, AAV-2 and AAV-6 is shown in box with waved lines.

Fig 3B is a detailed illustration of a 71 bp homologous region among AAV-1, AAV-2 and AAV-6 Nucleotides that differ among these serotypes are indicated by arrows.

Fig. 4A is a bar chart illustrating expression levels of human alpha 1 anti-trypsin (α1AT) in serum following delivery of hAAT via recombinant AAV-1 and recombinant AAV-2 viruses.

Fig. 4B is a bar chart illustrating expression levels of erythropoietin (epo) in serum following delivery of the epo gene via recombinant AAV-1 and recombinant AAV-2 viruses.

Fig. 5A is a bar chart illustrating expression levels of α1AT in liver following delivery of α1AT as described in Example 7.

Fig. 5B is a bar chart demonstrating expression levels of epo in liver following delivery of epo as described in Example 7.

Fig. 5C is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-1 following delivery of α1AT or epo to liver as described in Example 7.

Fig. 5D is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-2 following delivery of α1AT or epo to liver as described in Example 7.

Fig. 6A is a bar chart illustrating expression levels of α1AT in muscle following delivery of α1AT as described in Example 7.

Fig. 6B is a bar chart demonstrating expression levels of epo in muscle following delivery of epo as described in Example 7.

Fig. 6C is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-1 following delivery of α1AT or epo to muscle as described in Example 7.

Fig. 6D is a bar chart demonstrating neutralizing antibodies (NAB) directed to AAV-2 following delivery of α1AT or epo to muscle as described in Example 7.

Detailed Description of the Invention

The present invention provides novel nucleic acid sequences for an adeno--associated virus of serotype 1 (AAV-1). Also provided are fragments of these AAV-1 sequences. Among particularly desirable AAV-1 fragments are the inverted terminal repeat sequences (ITRs), rep and cap. Each of these fragments may be readily utilized, e.g., as a cassette, in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV-1 sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a cassette may contain the AAV-1 ITRs of the invention flanking a selected transgene. In another desirable embodiment, a cassette may contain the AAV-1 rep and/or cap proteins, e.g., for use in producing recombinant (rAAV) virus.

Thus, the AAV-1 sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors. The invention further provides nucleic acid molecules, gene delivery

vectors, and host cells which contain the AAV-1 sequences of the invention. Also provided a novel methods of gene delivery using AAV vectors.

As described herein, the vectors of the invention containing the AAV-1 capsid proteins of the invention are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

These and other embodiments and advantages of the invention are described in more detail below. As used throughout this specification and the claims, the term "comprising" is inclusive of other components, elements, integers, steps and the like.

I. AAV-1 NUCLEIC ACID AND PROTEIN SEQUENCES

The AAV-1 nucleic acid sequences of the invention include the DNA sequences of SEQ ID NO: 1 (Figs. 1A-1C), which consists of 4718 nucleotides. The AAV-1 nucleic acid sequences of the invention further encompass the strand which is complementary to SEQ ID NO: 1, as well as the RNA and cDNA sequences corresponding to SEQ ID NO: 1 and its complementary strand. Also included in the nucleic acid sequences of the invention are natural variants and engineered modifications of SEQ ID NO: 1 and its complementary strand. Such modifications include, for example, labels which are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with an analog.

Further included in this invention are nucleic acid sequences which are greater than 85%, preferably at least about 90%, more preferably at least about 95%, and most preferably at least about 98 - 99% identical or homologous to SEQ ID NO:1. The term "percent sequence identity" or "identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length sequence, or a fragment at least about nine nucleotides, usually at least about 20 - 24 nucleotides, at least about 28 - 32 nucleotides, and preferably at least about 36 or more nucleotides. There are a number of different

algorithms known in the art which can be used to measure nucleotide sequence identity. For instance, polynucleotide sequences can be compared using Fasta, a program in GCG Version 6.1. Fasta provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences (Pearson, 1990, herein incorporated by reference). For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference.

The term "substantial homology" or "substantial similarity," when referring to a nucleic acid or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 - 99% of the sequence.

Also included within the invention are fragments of SEQ ID NO: 1, its complementary strand, cDNA and RNA complementary thereto. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments which are of biological interest. Certain of these fragments may be identified by reference to Figs. 1A-1C. Examples of particularly desirable functional fragments include the AAV-1 inverted terminal repeat (ITR) sequences of the invention In contrast to the 145 nt ITRs of AAV-2, AAV-3, and AAV-4, the AAV-1 ITRs have been found to consist of only 143 nucleotides, yet advantageously are characterized by the T-shaped hairpin structure which is believed to be responsible for the ability of the AAV-2 ITRs to direct site-specific integration. In addition, AAV-1 is unique among other AAV serotypes, in that the 5' and 3' ITRs are identical. The full-length 5' ITR sequences of AAV-1 are provided at nucleotides l-143 of SEQ ID NO: 1 (Fig. 1A) and the full-length 3' ITR sequences of AAV-1 are provided at nt 4576-4718 of SEQ ID NO: 1 (Fig. 1C). One of skill in the art can readily utilize less than the full-length 5' and/or 3' ITR sequences for various purposes and may construct modified ITRs using conventional techniques, e.g., as described for AAV-2 ITRs in Samulski et al, Cell, 33:135-143 (1983).

Another desirable functional fragment of the AAV-1 genome is the P5 promoter of AAV-1 which has sequences unique among AAV P5 promoters, while maintaining critical regulatory elements and functions. This promoter is located within nt 236 - 299 of SEQ ID NO: 1 (Fig. 1A). Other examples of functional fragments of interest include the sequences at the junction of the rep/cap, e.g., the sequences spanning nt 2306-2223, as well as larger fragments which encompass this junction which may comprise 50 nucleotides on either side of this junction. Still other examples of functional fragments include the sequences encoding the rep proteins. Rep 78 is located in the region of nt 334 - 2306 of SEQ ID NO: 1; Rep 68 is located in the region of nt 334-2272, and contains an intron spanning nt 1924-2220 of SEQ ID NO: 1. Rep 52 is located in the region of nt 1007 - 2304 of SEQ ID NO. 1, rep 40 is located in the region of nt 1007 - 2272, and contains an intron spanning nt 1924-2246 of SEQ ID NO: 1. Also of interest are the sequences encoding the capsid proteins, VP 1 [nt 2223-4431 of SEQ ID NO. 1], VP2 [nt 2634-4432 of SEQ ID NO: 1] and VP3 [nt 2829-4432 of SEQ ID NO: 1]. Other fragments of interest may include the AAV-1 P19 sequences, AAV-1 P40 sequences, the rep binding site, and the terminal resolute site (TRS).

The invention further provides the proteins and fragments thereof which are encoded by the AAV-1 nucleic acids of the invention. Particularly desirable proteins include the rep and cap proteins, which are encoded by the nucleotide sequences identified above. These proteins include rep 78 [SEQ ID NO:5], rep 68 [SEQ ID NO:7], rep 52 [SEQ ID NO:9], rep 40 [SEQ ID NO: 11], vpl [SEQ ID NO: 13], vp2 [SEQ ID NO: 15], and vp3 [SEQ IID NO: 17] and functional fragments thereof while the sequences of the rep and cap proteins have been found to be closely related to those of AAV-6, there are differences in the amino acid sequences (see Table 1 below), as well as differences in the recognition of these proteins by the immune system. However, one of skill in the art may readily select other suitable proteins or protein fragments of biological interest. Suitably, such fragments are at least 8 amino acids in length. However, fragments of other desired lengths may be readily utilized.

Such fragments may be produced recombinantly or by other suitable means, e.g., chemical synthesis.

The sequences, proteins, and fragments of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

II. VIRAL VECTORS

In another aspect, the present invention provides vectors which utilize the AAV-1 sequences of the invention, including fragments thereof, for delivery of a heterologous gene or other nucleic acid sequences to a target cell. Suitably, these heterologous sequences (i.e., a transgene) encode a protein or gene product which is capable of being expressed in the target cell. Such a transgene may be constructed in the form of a "minigene" Such a "minigene" includes selected heterologous gene sequences and the other regulatory elements necessary to transcribe the gene and express the gene product in a host cell. Thus, the gene sequences are operatively linked to regulatory components in a manner which permit their transcription. Such components include conventional regulatory elements necessary to drive expression of the transgene in a cell containing the viral vector. The minigene may also contain a selected promoter which is linked to the transgene and located, with other regulatory elements, within the selected viral sequences of the recombinant vector.

Selection of the promoter is a routine matter and is not a limitation of this invention. Useful promoters may be constitutive promoters or regulated (inducible) promoters, which will enable control of the timing and amount of the transgene to be expressed. For example, desirable promoters include the cytomegalovirus (CMV) immediate early promoter/enhancer [see, e.g., Boshart et al, Cell, 41:521-530 (1985)], the Rous sarcoma virus LTR promoter/enhancer, and the chicken cytoplasmic β-actin promoter [T. A. Kost et al, Nucl. Acids Res., 11(23):8287 (1983)]. Still other desirable promoters are the albumin promoter and an AAV P5 promoter. Optionally, the selected promoter is used in conjunction with a heterologous enhancer, e.g., the β-

actin promoter may be used in conjunction with the CMV enhancer. Yet other suitable or desirable promoters and enhancers may be selected by one of skill in the art.

The minigene may also desirably contain nucleic acid sequences heterologous to the viral vector sequences including sequences providing signals required for efficient polyadenylation of the transcript (poly-A or pA) and introns with functional splice donor and acceptor sites. A common poly-A sequence which is employed in the exemplary vectors of this invention is that derived from the papovavirus SV-40. The poly-A sequence generally is inserted in the minigene downstream of the transgene sequences and upstream of the viral vector sequences. A common intron sequence is also derived from SV-40, and is referred to as the SV40 T intron sequence. A minigene of the present invention may also contain such an intron, desirably located between the promoter/enhancer sequence and the transgene. Selection of these and other common vector elements are conventional [see, e.g., Sambrook et al, "Molecular Cloning. A Laboratory Manual", 2d edit., Cold Spring Harbor Laboratory, New York (1989) and references cited therein] and many such sequences are available from commercial and industrial sources as well as from Genebank.

The selection of the transgene is not a limitation of the present invention. Suitable transgenes may be readily selected from among desirable reporter genes, therapeutic genes, and optionally, genes encoding immunogenic polypeptides. Examples of suitable reporter genes include β-galactosidase (β-gal), an alkaline phosphatase gene, and green fluorescent protein (GFP) Examples of therapeutic genes include, cytokines, growth factors, hormones, and differentiation factors, among others. The transgene may be readily selected by one of skill in the art. See, e.g., WO 98/09657, which identifies other suitable transgenes.

Suitably, the vectors of the invention contain, at a minimum, cassettes which consist of fragments of the AAV-1 sequences and proteins In one embodiment, a vector of the invention comprises a selected transgene, which is flanked by a 5' ITR and a 3' ITR, at least one of which is an AAV-1 ITR of the invention. Suitably,

vectors of the invention may contain a AAV-1 P5 promoter of the invention. In yet another embodiment, a plasmid or vector of the invention contains AAV-1 rep sequences. In still another embodiment, a plasmid or vector of the invention contains at least one of the AAV-1 cap proteins of the invention. Most suitably, these AAV-1-derived vectors are assembled into viral vectors, as described herein

A. AAV Viral Vectors

In one aspect, the present invention provides a recombinant AAV-1 viral vector produced using the AAV-1 capsid proteins of the invention. The packaged rAAV-1 virions of the invention may contain, in addition to a selected minigene, other AAV-1 sequences, or may contain sequences from other AAV serotypes.

Methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, e.g., K. Fisher et al, J. Virol., 70:520-532 (1993) and US Patent 5,478,745. In one suitable method, a selected host cell is provided with the AAV sequence encoding a rep protein, the gene encoding the AAV cap protein and with the sequences for packaging and subsequent delivery. Desirably, the method utilizes the sequences encoding the AAV-1 rep and/or cap proteins of the invention.

In one embodiment, the rep/cap genes and the sequences for delivery are supplied by co-transfection of vectors carrying these genes and sequences. In one currently preferred embodiment, a cis (vector) plasmid, a trans plasmid containing the rep and cap genes, and a plasmid containing the adenovirus helper genes are co--transfected into a suitable cell line, e.g., 293. Alternatively, one or more of these functions may be provided in trans via separate vectors, or may be found in a suitably engineered packaging cell line.

An exemplary cis plasmid will contain, in 5' to 3' order, AAV 5' ITR, the selected transgene, and AAV 3' ITR. In one desirable embodiment, at least one of the AAV ITRs is a 143 nt AAV-1 ITR. However, other AAV serotype ITRs may be readily selected. Suitably, the full-length ITRs are utilized. However, one of skill in

the art can readily prepare modified AAV ITRs using conventional techniques. Similarly, methods for construction of such plasmids is well known to those of skill in the art.

A trans plasmid for use in the production of the rAAV-1 virion particle may be prepared according to known techniques. In one desired embodiment, this plasmid contains the rep and cap proteins of AAV-1, or functional fragments thereof. Alternatively, the rep sequences may be from another selected AAV serotype.

The cis and trans plasmid may then be co-transfected with a wild-type helper virus (e.g., Ad2, Ad5, or a herpesvirus), or more desirably, a replication - defective adenovirus, into a selected host cell. Alternatively, the cis and trans plasmid may be co-transfected into a selected host cell together with a transfected plasmid which provides the necessary helper functions. Selection of a suitable host cell is well within the skill of those in the art and include such mammalian cells as 293 cells, HeLa cells, among others.

Alternatively, the cis plasmid and, optionally the trans plasmid, may be transfected into a packaging cell line which provides the remaining helper functions necessary for production of a rAAV containing the desired AAV-1 sequences of the invention. An example of a suitable packaging cell line, where an AAV-2 capsid is desired, is B-50, which stably expresses AAV-2 rep and cap genes under the control of a homologous P5 promoter. This cell line is characterized by integration into the cellular chromosome of multiple copies (at least 5 copies) of P5-rep-cap gene cassettes in a concatomer form. This B-50 cell line was deposited with the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209, on September 18, 1997 under Accession No. CRL-12401 pursuant to the provisions of the Budapest Treaty. However, the present invention is not limited as to the selection of the packaging cell line.

Exemplary transducing vectors based on AAV-1 capsid proteins have been tested both *in vivo and in vitro*, as described in more detail in Example 4. In these studies, it was demonstrated that recombinant AAV vector with an AAV-1 virion can transduce both mouse liver and muscle. These, and other AAV-1 based

gene therapy vectors which may be generated by one of skill in the art are beneficial for gene delivery to selected host cells and gene therapy patients since the neutralization antibodies of AAV-1 present in much of the human population exhibit different patterns from other AAV serotypes and therefore do not neutralize the AAV-1 virions. One of skill in the art may readily prepare other rAAV viral vectors containing the AAV-1 capsid proteins provided herein using a variety of techniques known to those of skill in the art. One may similarly prepare still other rAAV viral vectors containing AAV-1 sequence and AAV capsids of another serotype.

B Other Viral Vectors

One of skill in the art will readily understand that the AAV-1 sequences of the invention can be readily adapted for use in these and other viral vector systems for *in vitro, ex vivo or in vivo* gene delivery. Particularly well suited for use in such viral vector systems are the AAV-1 ITR sequences, the AAV-1 rep, the AAV-1 cap, and the AAV-1 P5 promoter sequences.

For example, in one desirable embodiment, the AAV-1 ITR sequences of the invention may be used in an expression cassette which includes AAV-1 5' ITR, a non-AAV DNA sequences of interest (e.g., a minigene), and 3' ITR and which lacks functional rep/cap. Such a cassette containing an AAV-1 ITR may be located on a plasmid for subsequent transfection into a desired host cell, such as the cis plasmid described above. This expression cassette may further be provided with an AAV capsid of a selected serotype to permit infection of a cell or stably transfected into a desired host cell for packaging of rAAV virions. Such an expression cassette may be readily adapted for use in other viral systems, including adenovirus systems and lentivirus systems. Methods of producing Ad/AAV vectors are well known to those of skill in the art. One desirable method is described in PCT/US95/14018. However, the present invention is not limited to any particular method.

Another aspect of the present invention is the novel AAV-1 P5 promoter sequences which are located in the region spanning nt 236 - 299 of SEQ ID NO: 1. This promoter is useful in a variety of viral vectors for driving expression of a desired transgene.

Similarly, one of skill in the art can readily select other fragments of the AAV-1 genome of the invention for use in a variety of vector systems. Such vectors systems may include, e.g., lentiviruses, retroviruses, poxviruses, vaccinia viruses, and adenoviral systems, among others. Selection of these vector systems is not a limitation of the present invention.

C Host Cells And Packaging Cell Lines

In yet another aspect, the present invention provides host cells which may be transiently transfected with AAV-1 nucleic acid sequences of the invention to permit expression of a desired transgene or production of a rAAV particle. For example, a selected host cell may be transfected with the AAV-1 P5 promoter sequences and/or the AAV-1 5' ITR sequences using conventional techniques. Providing AAV helper functions to the transfected cell lines of the invention results in packaging of the rAAV as infectious rAAV particles. Such cell lines may be produced in accordance with known techniques [see, e.g, US Patent No. 5,658,785], making use of the AAV-1 sequences of the invention.

Alternatively, host cells of the invention may be stably transfected with a rAAV expression cassette of the invention, and with copies of AAV-1 rep and cap genes. Suitable parental cell lines include mammalian cell lines and it may be desirable to select host cells from among non-simian mammalian cells. Examples of suitable parental cell lines include, without limitation, HeLa [ATCC CCL 2], A549 [ATCC Accession No. CCL 185], KB [CCL 17], Detroit [e.g., Detroit 510, CCL 72] and WI-38 [CCL 75] cells. These cell lines are all available from the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 USA. Other suitable parent cell lines may be obtained from other sources and may be used to construct stable cell lines containing the P5 and/or AAV rep and cap sequences of the invention.

Recombinant vectors generated as described above are useful for delivery of the DNA of interest to cells.

III. METHODS OF DELIVERING GENES VIA AAV-1 DERIVED VECTORS

In another aspect, the present invention provides a method for delivery of a transgene to a host which involves transfecting or infecting a selected host cell with a recombinant viral vector generated with the AAV-1 sequences (or functional fragments thereof) of the invention. Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

In one desirable embodiment, the invention provides a method for AAV--mediated delivery of a transgene to a host. This method involves transfecting or infecting a selected host cell with a recombinant viral vector containing a selected transgene under the control of sequences which direct expression thereof and AAV-1 capsid proteins.

Optionally, a sample from the host may be first assayed for the presence of antibodies to a selected AAV serotype. A variety of assay formats for detecting neutralizing antibodies are well known to those of skill in the art. The selection of such an assay is not a limitation of the present invention See, e.g., Fisher et al, Nature Med., 3(3):306-312 (March 1997) and W. C. Manning et al, Human Gene Therapy, 9:477-485 (March 1, 1998). The results of this assay may be used to determine which AAV vector containing capsid proteins of a particular serotype are preferred for delivery, e.g., by the absence of neutralizing antibodies specific for that capsid serotype.

In one aspect of this method, the delivery of vector with AAV-1 capsid proteins may precede or follow delivery of a gene via a vector with a different serotype AAV capsid protein. Thus, gene delivery via rAAV vectors may be used for repeat gene delivery to a selected host cell. Desirably, subsequently administered rAAV vectors carry the same transgene as the first rAAV vector, but the subsequently administered vectors contain capsid proteins of serotypes which differ from the first vector. For example, if a first vector has AAV-2 capsid proteins, subsequently administered vectors may have capsid proteins selected from among the other serotypes, including AAV-1, AAV-3A, AAV-3B, AAV-4 and AAV-6.

Thus, a rAAV-1-derived recombinant viral vector of the invention provides an efficient gene transfer vehicle which can deliver a selected transgene to a selected host cell *in vivo or ex vivo* even where the organism has neutralizing antibodies to one or more AAV serotypes. These compositions are particularly well suited to gene delivery for therapeutic purposes. However, the compositions of the invention may also be useful in immunization. Further, the compositions of the invention may also be used for production of a desired gene product *in vitro*.

The above-described recombinant vectors may be delivered to host cells according to published methods An AAV viral vector bearing the selected transgene may be administered to a patient, preferably suspended in a biologically compatible solution or pharmaceutically acceptable delivery vehicle. A suitable vehicle includes sterile saline. Other aqueous and non-aqueous isotonic sterile injection solutions and aqueous and non-aqueous sterile suspensions known to be pharmaceutically acceptable carriers and well known to those of skill in the art may be employed for this purpose

The viral vectors are administered in sufficient amounts to transfect the cells and to provide sufficient levels of gene transfer and expression to provide a therapeutic benefit without undue adverse effects, or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to the liver, oral, intranasal, intravenous, intramuscular, subcutaneous, intradermal, and other parental routes of administration. Routes of administration may be combined, if desired.

Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective human dosage of the viral vector is generally in the range of from about 1 ml to about 100 ml of solution containing concentrations of from about 1×10^9 to 1×10^{16} genomes virus vector. A preferred human dosage may be about 1×10^{13} to 1×10^{16} AAV genomes. The dosage will be adjusted to balance the therapeutic benefit against any side effects and

such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of the transgene can be monitored to determine the frequency of dosage resulting in viral vectors, preferably AAV vectors containing the minigene. Optionally, dosage regimens similar to those described for therapeutic purposes may be utilized for immunization using the compositions of the invention. For *in vitro* production, a desired protein may be obtained from a desired culture following transfection of host cells with a rAAV containing the gene encoding the desired protein and culturing the cell culture under conditions which permits expression. The expressed protein may then be purified and isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

The following examples illustrate several aspects and embodiments of the invention.

Example 1 - Generation of Infectious Clone of AAV-1

The replicated form DNA of AAV-1 was extracted from 293 cells that were infected by AAV-1 and wild type adenovirus type 5.

A. Cell Culture and Virus

AAV-free 293 cells and 84-31 cells were provided by the human application laboratory of the University of Pennsylvania. These cells were cultured in Dulbecco's Modified Eagle Medium with 10% fetal bovine serum (Hyclone), penicillin (100 U/ml) and streptomycin at 37°C in a moisturized environment supplied with 5% $C0_2$. The 84-31 cell line constitutively expresses adenovirus genes E1a, Elb, E4/ORF6, and has been described previously [K. J. Fisher, J. Virol., 70:520-532 (1996)]. AAV-1 (ATCC VR-645) seed stock was purchased from American Type Culture Collection (ATCC, Manassas, VA). AAV viruses were propagated in 293 cells with wild type Ad5 as a helper virus.

B Recombinant AAV Generation

The recombinant AAV viruses were generated by transfection using an adenovirus free method. Briefly, the cis plasmid (with AAV ITR), trans plasmid (with

AAV rep gene and cap gene) and helper plasmid (pFΔ13, with essential regions from the adenovirus genome) were simultaneously co-transfected into 293 cells in a ratio of 1:1:2 by calcium phosphate precipitation. The pFΔ13 helper plasmid has an 8 kb deletion in the adenovirus E2B region and has deletions in most of the late genes. This helper plasmid was generated by deleting the RsrII fragment from pFG140 (Microbix, Canada). Typically, 50 μg of DNA (cis:trans:PFΔ13 at ratios of 1:1:2, respectively) was transfected onto a 15 cm tissue culture dish. The cells were harvested 96 hours post-transfection, sonicated and treated with 0.5% sodium deoxycholate (37°C for 10 min). Cell lysates were then subjected to two rounds of a CsCl gradient. Peak fractions containing AAV vector were collected, pooled, and dialyzed against PBS before injecting into animals. To make rAAV virus with AAV-1 virion, the pAV1H or p5E18 (2/1) was used as the *trans* plasmid to provide rep and cap function.

For the generation of rAAV based on AAV-2, p5E18 was used as the *trans* plasmid since it greatly improved the rAAV yield. This plasmid, p5E18(2/2), expresses AAV-2 Rep and Cap and contains a P5 promoter relocated to a position 3' to the Cap gene, thereby minimizing expression of Rep78 and Rep68. The strategy was initially described by Li et al, J. Virol., 71:5236-5243 (1997). P5E18(2/2) was constructed in the following way The previously described pMMTV-trans vector (i.e., the mouse mammary tumor virus promoter substituted for the P5 promoter in an AAV-2-based vector) was digested with *Sma*I and *Cla*I, filled in with the Klenow enzyme, and then recircularized with DNA ligase. The resulting construct was digested with *Xba*I, filled in, and ligated to the blunt-ended BamHI-*Xba*I fragment from pCR-p5, constructed in the following way. The P5 promoter of AAV was amplified by PCR and the amplified fragment was subsequently cloned into pCR2.1 (Invitrogen) to yield pCR-P5. The helper plasmid pAV1H was constructed by cloning the *Bfa*I fragment of pAAV-2 into pBluescript II-SK(+) at the *Bcor*V and *Sma*I sites. The 3.0-kb *Xba*I-*Kpn*I fragment from p5E18(2/2), the 2.3-kb *Xba*I-*Kpn*I fragment from pAV1H, and the 1.7-kb KpnI fragment from p5E18(2/2) were incorporated into a separate plasmid P5E18(2/1), which contains AAV-2 Rep, AAV-1 Cap, and the

AAV-2 P5 promoter located 3' to the Cap gene. Plasmid p5E18(2/1) produced 10- to 20-fold higher quantities of the vector than pAV1H (i.e., 10^{12} genomes/50 15-cm^2 plates).

C. DNA Techniques

Hirt DNA extraction was performed as described in the art with minor modification [R.J. Samulski et al., Cell, 33:135-143 (1983)]. More particularly, Hirst solution without SDS was used instead of using original Hirt solution containing SDS. The amount of SDS present in the original Hirst solution was added after the cells had been fully suspended. To construct AAV-1 infectious clone, the Hirt DNA from AAV-1 infected 293 cells was repaired with Klenow enzyme (New England Biolabs) to ensure the ends were blunt. The treated AAV-1 Hirt DNA was then digested with *BamH*I and cloned into three vectors, respectively. The internal *BamH*I was cloned into pBlueScript II-SK+ cut with *BamH*I to get pAV1-BM. The left and right fragments were cloned into pBlueScript II-SK+ cut with *BamH*I + EcoRV to obtain pAV1-BL and pAV1-BR, respectively. The AAV sequence in these three plasmids were subsequently assembled into the same vector to get AAV-1 infectious clone pAAV-1. The helper plasmid for recombinant AAV-1 virus generation was constructed by cloning the Bfa I fragment of pAAV-1 into pBlueScript II-SK+ at the EcoRV site.

Analysis of the Hirt DNA revealed three bands, a dimer at 9.4 kb, a monomer at 4.7 kb and single-stranded DNA at 1.7 kb, which correlated to different replication forms of AAV-1. The monomer band was excised from the gel and then digested with *BamH*I. This resulted in three fragments of 1.1 kb, 0.8 kb and 2.8 kb. This pattern is in accordance with the description by Bantel-schaal and zur Hausen, Virol., 134(1):52-63 (1984). The 1.1 kb and 2.8 kb *Bam*HI fragments were cloned into pBlueScript-KS(+) at *BamH*I and EcoRV site. The internal 0.8 kb fragment was cloned into *BamH*I site of pBlueScript-KS(+).

These three fragments were then subcloned into the same construct to obtain a plasmid (pAAV-1) that contained the full sequence of AAV-1. The pAAV-1 was then tested for its ability to rescue from the plasmid backbone and package

infectious virus. The pAAV-1 was then transfected to 293 cells and supplied with adenovirus type as helper at MOI 10. The virus supernatant was used to reinfect 293 cells.

For Southern blot analysis, Hirt DNA was digested with *Dpn*I to remove bacteria-borne plasmid and probed with internal *BamH*I fragment of AAV-1. The membrane was then washed at high stringency conditions, which included: twice 30 minutes with 2X SSC, 0.1% SDS at 65°C and twice 30 minutes with 0.1X SSC, 0.1% SDS at 65°C. The membrane was then analyzed by both phosphor image and X-ray autoradiography. The results confirmed that pAAV-1 is indeed an infectious clone of AAV serotype 1.

Example 2 - Sequencing Analysis of AAV-1

The entire AAV-1 genome was then determined by automatic sequencing and was found to be 4718 nucleotides in length (Figs. 1A-1C). For sequencing, an ABI 373 automatic sequencer as used to determine the sequences for all plasmids and PCR fragments related to this study using the FS dye chemistry. All sequences were confirmed by sequencing both plus and minus strands. These sequences were also confirmed by sequencing two independent clones of pAV-BM, pAV-BL and pAV-BR. Since the replicated form of AAV-1 DNA served as the template for sequence determination, these sequences were also confirmed by sequencing a series of PCR products using original AAV-1 seed stock as a template.

The length of AAV-1 was found to be within the range of the other serotypes: AAV-3 (4726 nucleotides), AAV-4 (4774 nucleotides), AAV-2 (4681 nucleotides), and AAV-6 (4683 nucleotides).

The AAV-1 genome exhibited similarities to other serotypes of adeno-associated viruses. Overall, it shares more than 80% identity with other known AAV viruses as determined by the computer program Megalign using default settings [DNASTAR, Madison, WI]. The key features in AAV-2 can also be found in AAV-1. First, AAV-1 has the same type of inverted terminal repeat which is capable of forming T-shaped hairpin structures, despite the differences at the nucleotide level

(Figs. 2 and 3). The sequences of right ITRs and left ITRs of AAV-1 are identical. The AAV TR sequence is subdivided into A, A', B, B', C, C', D and D' [Bern, cited above].

These AAV ITR sequences are also virtually the same as those found in AAV-6 right ITR, there being one nucleotide difference in each of A and A' sequence, and the last nucleotide of the D sequence. Second, the AAV-2 rep binding motif [GCTCGCTCGCTCGCTG (SEQ ID NO: 20)] is well conserved. Such motif can also be found in the human chromosome 19 AAV-2 pre-integration region. Finally, non-structural and structural coding regions, and regulatory elements similar to those of other AAV serotypes also exist in AAV-1 genome.

Although the overall features of AAV terminal repeats are very much conserved, the total length of the AAV terminal repeat exhibits divergence. The terminal repeat of AAV-1 consists of 143 nucleotides while those of AAV-2, AAV-3, and AAV-4 are about 145 or 146 nucleotides. The loop region of AAV-1 ITR most closely resembles that of AAV-4 in that it also uses TCT instead of the TTT found in AAV-2 and AAV-3. The possibility of sequencing error was eliminated using restriction enzyme digestion, since these three nucleotides are part of the SacI site (gagctc, nt 69-74 of SEQ ID NO: 1). The p5 promoter region of AAV-1 shows more variations in nucleotide sequences with other AAV serotypes. However, it still maintains the critical regulatory elements. The two copies of YY1 [See, Fig. 1A-1C] sites seemed to be preserved in all known AAV serotypes, which have been shown to be involved in regulating AAV gene expression. In AAV-4, there are 56 additional nucleotides inserted between YY1 and E-box/USF site, while in AAV-1, there are 26 additional nucleotides inserted before the E-box/USF site. The p19 promoter, p40 promoter and polyA can also be identified from the AAV-1 genome by analogy to known AAV serotypes, which are also highly conserved.

Thus, the analysis of AAV terminal repeats of various serotypes showed that the A and A' sequence is very much conserved. One of the reasons may be the Rep binding motif $(GCTC)_3GCTG$ [SEQ ID NO: 20]. These sequences appear to be essential for AAV DNA replication and site-specific integration. The same sequence

has also been shown to be preserved in a monkey genome [Samulski, personal communication]. The first 8 nucleotides of the D sequence are also identical in all known AAV serotypes. This is in accordance with the observation of the Srivastava group that only the first 10 nucleotides are essential for AAV packaging [X.S. Wang et al, J. Virol., 71:3077-3082 (1997); X.S. Wang et al, J. Virol., 71:1140-1146 (1997)]. The function of the rest of the D sequences still remain unclear. They may be somehow related to their tissue specificities. The variation of nucleotide in B and C sequence may also suggest that the secondary structure of the ITRs is more critical for its biological function, which has been demonstrated in many previous publications.

Example 3 - Comparison of AAV-1 Sequences

The nucleotide sequences of AAV-1, obtained as described above, were compared with known AAV sequences, including AAV-2, AAV-4 and AAV-6 using DNA Star Megalign. This comparison revealed a stretch of 71 identical nucleotides shared by AAV-1, AAV-2 and AAV-6. See, Figs. 1A-1C.

This comparison further suggested that AAV-6 is a hybrid formed by homologous recombination of AAV-1 and AAV-2. See, Figs. 3A and 3B. These nucleotides divide the AAV-6 genome into two regions. The 5' half of AAV-6 of 522 nucleotides is identical to that of AAV-2 except in 2 positions. The 3' half of AAV-6 including the majority of the rep gene, complete cap gene and 3' ITR is 98% identical to AAV-1.

Biologically, such recombination may enable AAV-1 to acquire the ability to transmit through the human population. It is also interesting to note that the ITRs of AAV-6 comprise one AAV-1 ITR and one AAV-2 ITR The replication model of defective parvovirus can maintain this special arrangement. Studies on AAV integration have shown that a majority of AAV integrants carries deletions in at least one of the terminal repeats. These deletions have been shown to be able to be repaired through gene conversion using the other intact terminal repeat as a template. Therefore, it would be very difficult to maintain AAV-6 as a homogenous population

when an integrated copy of AAV-6 is rescued from host cells with helper virus infection. The AAV-6 with two identical AAV-2 ITRs or two identical AAV-1 ITRs should be the dominant variants. The AAV-6 with two AAV-1 ITRs has been observed by Russell's group [Rutledge, cited above (1998)]. So far there is no report on AAV-6 with two AAV-2 ITRs. Acquirement of AAV-2 P5 promoter by AAV-6 may have explained that AAV-6 have been isolated from human origin while AAV-1 with the same virion has not. The regulation of P5 promoter between different species of AAV may be different *in vivo*. This observation suggests the capsid proteins of AAV were not the only determinants for tissue specificity.

Although it is clear that AAV-6 is a hybrid of AAV-1 and AAV-2, AAV-6 has already exhibited divergence from either AAV-1 or AAV-2 There are two nucleotide differences between AAV-6 and AAV-2 in their first 450 nucleotides. There are about 1% differences between AAV-6 and AAV-1 in nucleotide levels from nucleotides 522 to the 3' end. There also exists a quite divergent region (nucleotide 4486-4593) between AAV-6 and AAV-1 (Figs. 1A-1C). This region does not encode any known proteins for AAVs. These differences in nucleotide sequences may suggest that AAV-6 and AAV-1 have gone through some evolution since the recombination took place. Another possible explanation is that there exists another variant of AAV-1 which has yet to be identified. So far, there is no evidence to rule out either possibility. It is still unknown if other hybrids (AAV-2 to AAV-4, etc.) existed in nature.

The coding region of AAV-1 was deduced by comparison with other known AAV serotypes. Table 1 illustrates the coding region differences between AAV-1 and AAV-6. The amino acid residues are deduced according to AAV-2.

With reference to the amino acid position of AAV-1, Table 1 lists the amino acids of AAV-1 which have been changed to the corresponding ones of AAV-6. The amino acids of AAV-1 are shown to the left of the arrow. Reference may be made to SEQ ID NO: 5 of the amino acid sequence of AAV-1 Rep 78 and to SEQ ID NO: 13 for the amino acid sequence of AAV-1 VP1.

Table 1

Coding region variations between AAV-1 and AAV-6

Rep protein (Rep78)			Cap protein (VP1)	
Position(s)	Amino acids		Position(s)	Amino acids
28	S→N		129	L→F
191	Q→H		418	E→D
192	H→D		531	E→K
308	E→D		584	F→L
			598	A→V
			642	N→H

It was surprising to see that the sequence of the AAV-1 coding region is almost identical to that of AAV-6 from position 452 to the end of coding region (99%). The first 508 nucleotides of AAV-6 have been shown to be identical to those of AAV-2 [Rutledge, cited above (1998)]. Since the components of AAV-6 genome seemed to be AAV-2 left ITR – AAV-2 p5 promoter – AAV-1 coding region – AAV-1 right ITR, it was concluded that AAV-6 is a naturally occurred hybrid between AAV-1 and AAV-2.

Example 4 - Gene Therapy Vector Based on AAV-1

Recombinant gene transfer vectors based on AAV-1 viruses were constructed by the methods described in Example 1. To produce a hybrid recombinant virus with AAV-1 virion and AAV-2 ITR, the AAV-1 trans plasmid (pAV1H) and the AAV-2 cis-lacZ plasmid (with AAV-2 ITR) were used. The AAV-2 ITR was used in this vector in view of its known ability to direct site-specific integration. Also constructed for use in this experiment was an AAV-1 vector carrying the green fluorescent protein (GFP) marker gene under the control of the immediate early promoter of CMV using pAV1H as the trans plasmid.

A. rAAV-1 Viruses Transfect Host Cells in Vitro

84-31 cells, which are subclones of 293 cells (which express adenovirus E1a, E1b) which stably express E4/ORF5, were infected with rAAV-1 GFP or rAAV-lacZ. High levels of expression of GFP and lacZ was detected in the cultured 84-31 cells. This suggested that rAAV-1 based vector was very similar to AAV-2 based vectors in ability to infect and expression levels.

B. rAAV-1 Viruses Transfect Cells in Vivo

The performance of AAV-1 based vectors was also tested *in vivo*. The rAAV-1 CMV-α1AT virus was constructed as follows. The EcoRI fragment of pAT85 (ATCC) containing human α1-antitrypsin (α1AT) cDNA fragment was blunted and cloned into PCR (Promega) at a SmaI site to obtain PCR-α1AT. The CMV promoter was cloned into PCR-α1AT at the XbaI site. The Alb-α1AT expression cassette was removed by XhoI and ClaI and cloned into pAV1H at the XbaI site This vector plasmid was used to generate AAV-1-CMV-α1AT virus used in the experiment described below.

For screening human antibodies against AAV, purified AAV virus is lysed with Ripa buffer (10 mM Tris pH 8.2, 1% Triton X-100, 1% SDS, 0.15 M NaCl) and separated in 10% SDS-PAGE gel. The heat inactivated human serum was used at a 1 to 1000 dilution in this assay. The rAAV-1 CMV-α1AT viruses were injected into Rag-1 mice through tail vein injection at different dosages. The concentration of human α1-antitrypsin in mouse serum was measured using ELISA. The coating antibody is rabbit anti-human human α1-antitrypsin (Sigma). The goat-antihuman α1-antitrypsin (Sigma) was used as the primary detection antibodies. The sensitivity of this assay is around 0.3 ng/ml to 30 ng/ml. The expression of human α-antitrypsin in mouse blood can be detected in a very encouraging level. This result is shown in Table 2.

Table 2

Human Antitrypsin Expressed in Mouse Liver

Amount of virus injected	Week 2 (ng/ml)	Week 4 (ng/ml)
$2x10^{10}$ genomes	214.2	171.4
$1x10^{10}$ genomes	117.8	109.8
$5x10^{10}$ genomes	64.5	67.8
$2.5x10^{10}$ genomes	30.9	58.4

rAAV-1 CMV-lacZ viruses were also injected into the muscle of C57BL6 mice and similar results were obtained. Collectively, these results suggested that AAV-1 based vector would be appropriate for both liver and muscle gene delivery.

Example 5 - Neutralizing Antibodies Against AAV-1

Simple and quantitative assays for neutralizing antibodies (NAB) to AAV-1 and AAV-2 were developed with recombinant vectors. A total of 33 rhesus monkeys and 77 normal human subjects were screened.

A. *Nonhuman Primates*

Wild-caught juvenile rhesus monkeys were purchased from Covance (Alice, Tex.) and LABS of Virginia (Yemassee, SC) and kept in full quarantine. The monkeys weighed approximately 3 to 4 kg. The nonhuman primates used in the Institute for Human Gene Therapy research program are purposefully bred in the United States from specific-pathogen-free closed colonies. All vendors are US Department of Agriculture class A dealers. The rhesus macaques are therefore not infected with important simian pathogens, including the tuberculosis agent, major simian lentiviruses (simian immunodeficiency virus and simian retroviruses), and cercopithecine herpesvirus. The animals are also free of internal and external parasites. The excellent health status of these premium animals minimized the potential for extraneous variables. For this study, serum was obtained from monkeys prior to initiation of any protocol.

NAB titers were analyzed by assessing the ability of serum antibody to inhibit the transduction of reporter virus expressing green fluorescent protein (GFP) (AAV1-GFP or AAV2-GFP) into 84-31 cells. Various dilutions of antibodies preincubated with reporter virus for 1 hour at 37°C were added to 90% confluent cell cultures. Cells were incubated for 48 hours and the expression of green fluorescent protein was measured by FluoroImaging (Molecular Dynamics). NAB titers were calculated as the highest dilution at which 50% of the cells stained green.

Analysis of NAB in rhesus monkeys showed that 61% of animals tested positive for AAV-1; a minority (24%) has NAB to AAV-2. Over one-third of animals had antibodies to AAV-1 but not AAV-2 (i.e., were monospecific for AAV-1), whereas no animals were positive for AAV-2 without reacting to AAV-1. These data support the hypothesis that AAV-1 is endemic in rhesus monkeys. The presence of true AAV-2 infections in this group of nonhuman primates is less clear, since cross-neutralizing activity of an AAV-1 response to AAV-2 can not be ruled out. It is interesting that there is a linear relationship between AAV-2 NAB and AAV-1 NAB in animals that had both.

B. *Humans*

For these neutralization antibody assays, human serum samples were incubated at 56°C for 30 min to inactivate complement and then diluted in DMEM. The virus (rAAV or rAd with either lacZ or GFP) was then mixed with each serum dilution (20X, 400X, 2000X, 4000X, etc.) and incubated for 1 hour at 37°C before applied to 90% confluent cultures of 84-31 cells (for AAV) or Hela cells (for adenovirus) in 96-well plates. After 60 minutes of incubation at culture condition, 100 µl additional media containing 20% FCS was added to make final culture media containing 10% FCS.

The result is summarized in Table 3.

Table 3

Adenovirus	AAV-1	AAV-2	# of samples	Percentage
-	-	-	41	53.2%
+	-	-	16	20.8%
-	+	-	0	0.0%
-	-	+	2	2.6%
-	+	+	2	2.6%
+	-	+	3	3.9%
+	+	-	0	0.0%
+	+	+	13	16.9%
		Total	77	100%

The human neutralizing antibodies against these three viruses seemed to be unrelated since the existence of neutralizing antibodies against AAV are not indications for antibodies against adenovirus. However, AAV requires adenovirus as helper virus, in most of the cases, the neutralizing antibodies against AAV correlated with the existence of neutralizing antibodies to adenovirus. Among the 77 human serum samples screened, 41% of the samples can neutralize the infectivity of recombinant adenovirus based on Ad5. 15/77 (19%) of serum samples can neutralize the transduction of rAAV-1 while 20/77 (20%) of the samples inhibit rAAV-2 transduction at 1 to 80 dilutions or higher. All serum samples positive in neutralizing antibodies for AAV-1 in are also positive for AAV-2. However, there are five (6%) rAAV-2 positive samples that failed to neutralize rAAV-1. In samples that are positive for neutralizing antibodies, the titer of antibodies also varied in the positive ones. The results from screening human sera for antibodies against AAVs supported the conclusion that AAV-1 presents the same epitome as that of AAV-2 to interact

with cellular receptors since AAV-1 neutralizing human serums can also decrease the infectivity of AAV-2. However, the profile of neutralizing antibodies for these AAVs is not identical, there are additional specific receptors for each AAV serotype.

Example 6 - Recombinant AAV Viruses Exhibit Tissue Tropism

The recombinant AAV-1 vectors of the invention and the recombinant AAV-2 vectors [containing the gene encoding human α1-antitrypsin (α1AT) or murine erythropoietin (Epo) from a cytomegalovirus-enhanced β-actin promoter (CB)] were evaluated in a direct comparison to equivalent copies of AAV-2 vectors containing the same vector genes.

Recombinant viruses with AAV-1 capsids were constructed using the techniques in Example 1 To make rAAV with AAV-1 virions, pAV1H or p5E18 (2/1) was used as the *trans* plasmid to provide Rep and Cap functions. For the generation of the rAAV based on AAV-2, p5E18(2/2) was used as the *trans* plasmid, since it greatly improved the rAAV yield. [Early experiments indicated similar *in vivo* performances of AAV-1 vectors produced with pAV1H and p5E19 (2/1). All subsequent studies used AAV-1 vectors derived from p5E18(2/1) because of the increased yield.]

Equivalent stocks of the AAV-1 and AAV-2 vectors were injected intramuscularly (5×10^{10} genomes) or liver via the portal circulation (1×10^{11} genomes) into immunodeficient mice, and the animals (four groups) were analyzed on day 30 for expression of transgene. See, Figs. 4A and 4B.

AAV-2 vectors consistently produced 10- to 50-fold more serum erythropoietin or α1-antitrypsin when injected into liver compared to muscle. (However, the AAV-1-delivered genes did achieve acceptable expression levels in the liver.) This result was very different from that for AAV-1 vectors, with which muscle expression was equivalent to or greater than liver expression In fact, AAV-1 outperformed AAV-2 in muscle when equivalent titers based on genomes were administered.

Example 7 - Gene Delivery via rAAV-1

C57BL/6 mice (6- to 8-week old males, Jackson Laboratories) were analyzed for AAV mediated gene transfer to liver following intrasplenic injection of vector (i.e., targeted to liver). A total of 10^{11} genome equivalents of rAAV-1 or rAAV-2 vector were injected into the circulation in 100 µl buffered saline. The first vector contained either an AAV-1 capsid or an AAV-2 capsid and expressed α1AT under the control of the chicken β-actin (CB) promoter. Day 28 sera were analyzed for antibodies against AAV-1 or AAV-2 and serum α1AT levels were checked. Animals were then injected with an AAV-1 or AAV-2 construct expressing erythropoietin (Epo, also under the control of the CB promoter). One month later sera was analyzed for serum levels of Epo. The following groups were analyzed (Figs. 5A-5D).

In Group 1, vector 1 was AAV-2 expressing α1AT and vector 2 was AAV-2 expressing Epo Animals generated antibodies against AAV-2 following the first vector administration which prevented the readministration of the AAV-2 based vector. There was no evidence for cross-neutralizing the antibody to AAV-1.

In Group 2, vector 1 was AAV-1 expressing α1AT while vector 2 was AAV-1 expressing Epo. The first vector administration did result in significant α1AT expression at one month associated with antibodies to neutralizing antibodies to AAV-1. The animals were not successfully readministered with the AAV-1 Epo expressing construct.

In Group 3, the effectiveness of an AAV-2 vector expressing Epo injected into a naive animal was measured. The animals were injected with PBS and injected with AAV-2 Epo vector at day 28 and analyzed for Epo expression one month later. The neutralizing antibodies were evaluated at day 28 so we did not expect to see anything since they received PBS with the first vector injection. This shows that in naive animals AAV-2 is very efficient at transferring the Epo gene as demonstrated by high level of serum Epo one month later.

Group 4 was an experiment similar to Group 3 in which the animals originally received PBS for vector 1 and then the AAV-1 expressing Epo construct 28 days later. At the time of vector injection, there obviously were no antibodies to either

AAV-1 or AAV-2. The AAV-1 based vector was capable of generating significant expression of Epo when measured one month later.

Group 5 is a cross-over experiment where the initial vector is AAV-2 expressing α1AT followed by the AAV-1 construct expressing Epo. The animals, as expected, were efficiently infected with the AAV-2 vector expressing α1AT as shown by high levels of the protein in blood at 28 days. This was associated with significant neutralizing antibodies to AAV-2. Importantly, the animals were successfully administered AAV-1 following the AAV-2 vector as shown by the presence of Epo in serum 28 days following the second vector administration. At the time of this vector administration, there was high level AAV-2 neutralizing antibodies and very low cross-reaction to AAV-1. The level of Epo was slightly diminished possibly due to a small amount of cross-reactivity. Group 6 was the opposite cross-over experiment in which the initial vector was AAV-1 based, whereas the second experiment was AAV-2 based. The AAV-1 vector did lead to significant gene expression of α1AT, which also resulted in high level AAV-1 neutralizing antibody. The animals were very efficiently administered AAV-2 following the initial AAV-1 vector as evidenced by high level Epo.

A substantially identical experiment was performed in muscle in which 5×10^{10} genomes were injected into the tibialis anterior of C57BL/6 mice as a model for muscle directed gene therapy. The results are illustrated in Figs. 6A-6D and are essentially the same as for liver.

In summary, this experiment demonstrates the utility of using an AAV-1 vector in patients who have pre-existing antibodies to AAV-2 or who had initially received an AAV-2 vector and need readministration.

Example 8 - Construction of Recombinant Viruses Containing AAV-1 ITRs

This example illustrates the construction of recombinant AAV vectors which contain AAV-1 ITRs of the invention.

An AAV-1 cis plasmid is constructed as follows. A 160 bp Xho-NruI AAV-1 fragment containing the AAV-1 5' ITR is obtained from pAV1-BL. pAV1-BL was

generated as described in Example 1. The Xho-NruI fragment is then cloned into a second pAV1-BL plasmid at an XbaI site to provide the plasmid with two AAV-1 ITRs. The desired transgene is then cloned into the modified pAV-1BL at the NruI and BamHI site, which is located between the AAV-1 ITR sequences. The resulting AAV-1 cis plasmid contains AAV-1 ITRs flanking the transgene and lacks functional AAV-1 rep and cap.

Recombinant AAV is produced by simultaneously transfecting three plasmids into 293 cells. These include the AAV-1 cis plasmid described above; a trans plasmid which provides AAV rep/cap functions and lacks AAV ITRs; and a plasmid providing adenovirus helper functions. The rep and/or cap functions may be provided in trans by AAV-1 or another AAV serotype, depending on the immunity profile of the intended recipient Alternatively, the rep or cap functions may be provided in cis by AAV-1 or another serotype, again depending on the patient's immunity profile.

In a typical cotransfection, 50 μg of DNA (cis:trans:helper at ratios of 1:1:2, respectively) is transfected onto a 15 cm tissue culture dish. Cells are harvested 96 hours post transfection, sonicated and treated with 0.5% sodium deoxycholate (37° for 10 min). Cell lysates are then subjected to 2-3 rounds of ultracentrifugation in a cesium gradient. Peak fractions containing rAAV are collected, pooled and dialyzed against PBS. A typical yield is 1×10^{13} genomes/10^9 cells.

Using this method, one recombinant virus construct is prepared which contains the AAV-1 ITRs flanking the transgene, with an AAV-1 capsid. Another recombinant virus construct is prepared with contains the AAV-1 ITRs flanking the transgene, with an AAV-2 capsid.

All publications cited in this specification are incorporated herein by reference. While the invention has been described with reference to a particularly preferred embodiments, it will be appreciated that modifications can be made without departing from the spirit of the invention Such modifications are intended to fall within the scope of the claims.

What is claimed is.

1. An isolated AAV-1 nucleic acid molecule comprising a sequence selected from the group consisting of:

(a) SEQ ID NO: 1;

(b) a DNA sequence complementary to SEQ ID NO: 1;

(c) cDNA complementary to (a) or (b); and

(d) RNA complementary to any of (a) to (c).

2. A nucleic acid molecule comprising an AAV-1 inverted terminal repeat (ITR) sequence selected from the group consisting of:

(a) nt 1 to 143 of SEQ ID NO: 1;

(b) nt 4576 to 4718 of SEQ ID NO: 1;

(c) a nucleic acid sequence complementary to (a) or (b); and

(d) a functional fragment of (a), (b), or (c).

3. A recombinant vector comprising a 5' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:

(a) nt 1 to 143 of SEQ ID NO: 1;

(b) a nucleic acid sequence complementary to (a); and

(c) a functional fragment of (a) or (b).

4. The recombinant vector according to claim 3, wherein said vector further comprises a 3' AAV-1 ITR.

5. A recombinant vector comprising a 3' AAV-1 inverted terminal repeat (ITR) and a selected transgene, wherein said ITR has the sequence selected from the group consisting of:

(a) nt 4576 to 4718 of SEQ ID NO: 1;

(b) a nucleic acid sequence complementary to (a); and

(c) a functional fragment of (a) or (b).

6. The recombinant vector according to claim 5, wherein said vector further comprises a 5' AAV-1 ITR.

7. The recombinant vector according to any of claims 3-6, wherein said vector further comprises AAV-1 capsid proteins having the sequence of SEQ ID NO: 13, 15 or 17 or functional fragments thereof.

8. The recombinant vector according to any of claims 3-6, wherein said vector further comprises adenovirus sequences.

9. A recombinant vector comprising an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1 or a functional fragment thereof.

10. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said cap coding region comprises at least one member is selected from the group consisting of:

(a) vp1, nt 2223 to 4431 of SEQ ID NO: 1;

(b) vp2, nt 2634 to 4432 of SEQ ID NO. 1; and

(c) vp3, nt 2829 to 4432 of SEQ ID NO: 1.

11. A nucleic acid molecule encoding AAV-1 helper functions, said molecule comprising an AAV rep coding region and an AAV cap coding region, wherein said rep coding region comprises an AAV-1 rep coding region comprising at least one member selected from the group consisting of:

(a) rep 78, nt 335 to 2304 of SEQ ID NO: 1;

(b) rep 68, nt 335 to 2272 of SEQ ID NO: 1 or the cDNA corresponding thereto,

(c) rep 52, nt 1007 to 2304 of SEQ ID NO: 1; and

(d) rep 40, nt 1007 to 2272 of SEQ ID NO: 1 or the cDNA corresponding thereto.

12. A host cell transduced with a recombinant viral vector according to any of claims 3-6.

13. A host cell transduced with a nucleic acid molecule according to any of claims 1, 2, 10 or 11.

14. A host cell stably transduced with an AAV-1 P5 promoter having the sequence of nt 236 to 299 of SEQ ID NO: 1.

15. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to any of claims 3-6.

16. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 7.

17. A pharmaceutical composition comprising a carrier and a virus comprising the vector according to claim 8.

18. A method for AAV-mediated delivery of a transgene comprising the step of delivering to a host cell an AAV virion which comprises:

(a) a capsid comprising at least one capsid protein encoded by an AAV-1 cap gene; and

(b) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

19. A method for AAV-mediated delivery of a transgene to a host comprising the steps of:

(a) assaying a sample from the host to determine the presence of neutralizing antibodies specific against any serotype of AAV; and

(b) delivering to the host an AAV virion which comprises:

(i) a capsid comprising at least one capsid protein encoded by a cap gene of an AAV serotype against which the host has no antibodies as determined in step (a); and

(ii) a DNA molecule comprising a transgene under the control of regulatory sequences directing its expression.

20. The method according to claim 19, comprising the additional step of repeating steps (a) and (b).

21. Use of an AAV virion which comprises a capsid comprising (a) at least one capsid protein encoded by a cap gene of an AAV serotype against which the host has antibodies, and (b) a DNA molecule comprising a transgene operably linked to regulatory sequences directing its expression,

in the preparation of a medicament for delivery of a transgene to a host, wherein said host has no preexisting neutralizing antibodies against the AAV serotype of said cap gene.

22. A method for delivery of a transgene comprising the step of delivering to a host cell a recombinant virus comprising a recombinant vector according to any of claims 3-8.

23. A method for producing a selected gene product comprising the steps of transfecting a mammalian cell with the molecule according to claim 1 or a functional fragment thereof and culturing said cell under conditions suitable to express said gene product.

ABSTRACT OF THE DISCLOSURE

The nucleic acid sequences of adeno-associated virus (AAV) serotype 1 are provided, as are vectors and host cells containing these sequences and functional fragments thereof. Also provided are methods of delivering genes via AAV-1 derived vectors.

FIG 1A

```
AAV-1 ttgcccactccctctctgcgcgctcgctcgctcggtggggcctgcggaccaaaggtccgc   60
AAV-2 ...g.....................................ac..a....g.gc.........gc.   60
AAV-6 ...g.....................................ac..a....g.gc.........gc.   60

                                                  Rep binding site
AAV-1 agacggcagagctctgctctgccggccccaccgagcgagcgagcgcgcagagagggagtg   120
AAV-2 c....c.c.g...t...c.g.g.....t..gt.....................          120
AAV-6 c....c.c.g...t...c.g.g.....t..gt.....................          120

      TRS➘
AAV-1 ggcaactccatcactaggggtaaTCGCGAAGCGCCTCCCACGCTGCCGCGTCAGCGCTGA   180
AAV-2 .c.....................--..ct.G..G.----------.TG.A...G----...   163
AAV-6 .c.....................--..ct.G..G.----------.TG.A...G----...   163

                                                  E box/USF
AAV-1 CGTAAATTACGTCATAGGG---GAGTGGTCCTGTATTAGCTGTCACGTGAGTGCTTTTGC   237
AAV-2 ...G..............TTA.G.A.............AG........-.....-.....   222
AAV-6 ...G..............TTA.G.A.............AG........-.....-.....   222

          YY1                                     P5/TATA
AAV-1 GACATTTTGCGACACCACGTGGCCATTTAGGGTATATATGGCCGAGTGAGCGAGCAGGAT   297
AAV-2 ................T....T..CGCT......T..A.C..........AC.....G.   282
AAV-6 ................T....T..CGCT......T..A.C..........AC.....G.   282

          YY1/p5 RNA                              Rep 78/68
AAV-1 CTCCATTTTGAC-CGCGAAATTTGAACGAGCAGCAGCCATGCCGGGCTTCTACGAGATCG   356
AAV-2 ...........AG..G..GG........C.....C...........G..T........T.   342
AAV-6 ...........AG..G..GG........C.....-...........G..T........T.   341

AAV-1 TGATCAAGGTGCCGAGCGACCTGGACGAGCACCTGCCGGGCATTTCTGACTCGTTTGTGA   416
AAV-2 ....T.....C..C........T....G...T.....C............AGC.......   402
AAV-6 ....T.....C..C........T........T.....C............AGC.......   401

AAV-1 GCTGGGTGGCCGAGAAGGAATGGGAGCTGCCCCCGGATTCTGACATGGATCTGAATCTGA   476
AAV-2 A.........................T....G..A.........................   462
AAV-6 A.........................T....G..A.........................   461

AAV-1 TTGAGCAGGCACCCCTGACCGTGGCCGAGAAGCTGCAGCGCGACTTCCTGGTCCAATGGC   536
AAV-2 ..........................................T...ACGG......      522
AAV-6 ..........................................G....               521

AAV-1 GCCGCGTGAGTAAGGCCCCGGAGGCCCTCTTCTTTGTTCAGTTCGAGAAGGGCGAGTCCT   596
AAV-2 ....T.....................T........G..A..T........A...AG..   582
AAV-6 ..........................................                    581

AAV-1 ACTTCCACCTCCATATTCTGGTGGAGACCACGGGGGTCAAATCCATGGTGCTGGGCCGCT   656
AAV-2 ........A.G..CG.G..C.....A.....C.....G...........TT....A..T.   642
AAV-6 ..........................................                    641

AAV-1 TCCTGAGTCAGATTAGGGACAAGCTGGTGCAGACCATCTACCGCGGGATCGAGCCGACCC   716
AAV-2 .............C.C..A..A...A.T....GA..T.....................TT   702
AAV-6 ..........................................                    701

AAV-1 TGCCCAACTGGTTCGCGGTGACCAAGACGCGTAATGGCGCCGGAGGGGGGAACAAGGTGG   776
AAV-2 ....A.............C..A.....CA.A.............C.............      762
AAV-6 ..........................................                    761
```

FIG 1B

```
AAV-1 TGGACGAGTGCTACATCCCCAACTACCTCCTGCCCAAGACTCAGCCCGAGCTGCAGTGGG  836
AAV-2 ....T.................T...T.G..C.....A..C.....T.....C.......  822
AAV-6 .....................................................          821

                          P19/TATA          P19 RNA↘
AAV-1 CGTGGACTAACATGGAGGAGTATATAAGCGCCTGTTTGAACCTGGCCGAGCGCAAACGGC  896
AAV-2 ..........T.....AC.....T.......C.....G..T..CA.G.....T......T  882
AAV-6 ..........C.....GG.....A.......G.....A..C..GG.C.............  881

AAV-1 TCGTGGCGCAGCACCTGACCCACGTCAGCCAGACCCAGGAGCAGAACAAGGAGAATCTGA  956
AAV-2 .G...........T.....G.....GTCG.....G.............A.......A..   942
AAV-6 ..........CG.....................................           941

                                                  Rep 52/40
AAV-1 ACCCCAATTCTGACGCGCCTGTCATCCGGTCAAAAACCTCCGCGCGCTACATGGAGCTGG 1016
AAV-2 .T..........T.....G..G...A.A........T..A..CA.G.............  1002
AAV-6 ..............................A.....................          1001

AAV-1 TCGGGTGGCTGGTGGACCGGGGCATCACCTCCGAGAAGCAGTGGATCCAGGAGGACCAGG 1076
AAV-2 ..........C......AA...G..T.....G.....................------  1062
AAV-6 ------------------------------------------------------------ 1061

AAV-1 CCTCGTACATCTCCTTCAACGCCGCTTCCAACTCGCGGTCCCAGATCAAGGCCGCTCTGG 1136
AAV-2 ....A.............T..G..C.................A........T..CT...  1122
AAV-6 ------------------------------------------------------------ 1121

AAV-1 ACAATGCCGGCAAGATCATGGCGCTGACCAAATCCGCGCCCGACTACCTGGTAGGCCCCG 1196
AAV-2 .......G..A.....T...AGC.....T...A....C..............G....AGC  1182
AAV-6 ------------------------------------------------------------ 1181

AAV-1 CTCCGCCCGCGGACATTAAAACCAACCGCATCTACCGCATCCTGGAGCTGAACGGCTACG 1256
AAV-2 AG..CGTG.A.......TCC.G...T..G..T..TAAA..TT....A..A.....G....  1242
AAV-6 ..........C.....................T.....------------------------  1241

AAV-1 AACCTGCCTACGCCGGCTCCGTCTTTCTCGGCTGGGCCCAGAAAAGGTTCGGGAAGCGCA 1316
AAV-2 .T..CCAA..T..G.CT...........G..A......AC.....A......C...A.G.  1302
AAV-6 .C.....................................................A..A....  1301

AAV-1 ACACCATCTGGCTGTTTGGGCCGGCCACCACGGGCAAGACCAACATCGCGGAAGCCATCG 1376
AAV-2 ......................T..A..T..C..G.................G.....A.  1362
AAV-6 ------------------------------------------------------------ 1361

AAV-1 CCCACGCCGTGCCCTTCTACGGCTGCGTCAACTGGACCAATGAGAACTTTCCCTTCAATG 1436
AAV-2 .....A.T.............G.....A.....................------------C.  1422
AAV-6 ------------------------------------------------------------C.  1421

AAV-1 ATTGCGTCGACAAGATGGTGATCTGGTGGGAGGAGGGCAAGATGACGGCCAAGGTCGTGG 1496
AAV-2 .C..T.....................G........C.............  1482
AAV-6 ------------------------------------------------------------ 1481

AAV-1 AGTCCGCCAAGGCCATTCTCGGCGGCAGCAAGGTGCGCGTGGACCAAAAGTGCAAGTCGT 1556
AAV-2 ....G.....A..........A..A.....G..A........C.  1542
AAV-6 ------------------------------------------------------------ 1541

AAV-1 CCGCCCAGATCGACCCCACCCCCGTGATCGTCACCTCCAACACCAACATGTGCGCCGTGA 1616
AAV-2 .G........A.....G..T.....  1602
AAV-6 ------------.T.....  1601
```

FIG 1C

```
AAV-1 TTGACGGGAACAGCACCACCTTCGAGCACCAGCAGCCGTTGCAGGACCGGATGTTCAAAT 1676
AAV-2 ..........TCA..G........A..................A.............. 1662
AAV-6 ..................................................... 1661

AAV-1 TTGAACTCACCCGCCGTCTGGAGCATGACTTTGGCAAGGTGACAAAGCAGGAAGTCAAAG 1740
AAV-2 ......................T...........G.....C..C.............. 1722
AAV-6 ..................................................... 1721

AAV-1 AGTTCTTCCGCTGGGCGCAGGATCACGTGACCGAGGTGGCGCATGAGTTCTACGTCAGAA 1796
AAV-2 .C..T.....G.....AA..........GTT.......A......A.........A.. 1782
AAV-6 ..................................................... 1781

                                          P40/TATA
AAV-1 AGGGTGGAGCCAACAAAAGACCCGCCCCCGATGACGCGGATAAAAGCGAGCCCAAGCGGG 1856
AAV-2 ............G..............AG......A....T...T........A.... 1842
AAV-6 ..............G.......................................... 1841

                  P40 RNA↘
AAV-1 CCTGCCCCTCAGTCGCGGATCCATCGACGTCAGACGCGGAAGGAGCTCCGGTGGACTTTG 1916
AAV-2 TGC..GAG.....T...C.G.........................---..T..A.CA...AC. 1899
AAV-6 ..................................................... 1901

                  ▼
AAV-1 CCGACAGGTACCAAAACAAATGTTCTCGTCACGCGGGCATGCTTCAGATGCTGTTTCCCT 1976
AAV-2 .A.............................T.......AA..T.............. 1959
AAV-6 ..................................................... 1961

AAV-1 GCAAGACATGCGAGAGAATGAATCAGAATTTCAACATTTGCTTCACGCACGGGACGAGAG 2036
AAV-2 ...GACA.........................CA..T..C........T.....ACA..A.. 2019
AAV-6 ....A.....................................................C.... 2021

AAV-1 ACTGTTCAGAGTGCTTCCCCGGCGTGTCAGAATCTCAACCGGTC---GTCAGAAAGAGGA 2093
AAV-2 ......T.........T..---.....................C..TTCT...GTC..A.A.G 2076
AAV-6 ..........A..T.....................................--.......... 2078

AAV-1 CGTATCGGAAACTCTGTGCCATTCATCATCTGCTGGGGCGGGCTCCCGAGATTGCTTGCT 2153
AAV-2 ......A......G..CTA..........A.CA....AAA..TG..A..---C......A 2133
AAV-6 ..................................................... 2138

                                                    Rep 78 stop
AAV-1 CGGCCTGCGATCTGGTCAACGTGGACCTGGATGACTGTGTTTCTGAGCAATAAATGACTT 2213
AAV-2 .T..................T.....TT..........CA.C.T...A..........T.. 2193
AAV-6 ........................T.............................. 2193

                ∇  VP1                                  ∇                                  Rep 68 stop
AAV-1 AAACCAGGTATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAG 2273
AAV-2 ...T.....................................................CT........A 2253
AAV-6 .....................................................AC........G 2258

AAV-1 GGCATTCGCGAGTGGTGGGACTTGAAACCTGGAGCCCCGAAGCCCAAAGCCAACCAGCAA 2333
AAV-2 ..A..AA.AC........A.GC.C.........CC.A..ACCA..A..GC..GCAG...GG 2313
AAV-6 ..............................A.................. 2318

AAV-1 AAGCAGGACGACGGCCGGGGTCTGGTGCTTCCTGGCTACAAGTACCTCGGACCCTTCAAC 2393
AAV-2 C.TA........A..A.......T...........G.......................... 2373
AAV-6 ............G..C.......G...........C.......................... 2378
```

FIG 1D

```
AAV-1 GGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCAGCGGCCCTCGAGCACGACAAG 2453
AAV-2 ..............A.....G.......A...A.....C...................A 2433
AAV-6 ..............................T.......................... 2438

AAV-1 GCCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCGGTATAACCACGCCGAC 2513
AAV-2 ..........G.......G.CAGC..A.....C........CAA...C............ 2493
AAV-6 ..................A.AGCG..T.....T........GCG...T............ 2498

AAV-1 GCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGCA 2573
AAV-2 ..G..............C..TA.............................A...... 2553
AAV-6 ..C..............T..GC.............................G...... 2558

AAV-1 GTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGTCTGGTTGAGGAAGGCGCTAAG 2633
AAV-2 ..........G..A...A.......T........G..C............CCT.T.... 2613
AAV-6 ..................A..............T.T................T..... 2618

      VP2
AAV-1 ACGGCTCCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAAGAGCCAGACTCCTCCTCG 2693
AAV-2 ........G.....A..GA.G...........C..T..TGTG.................. 2673
AAV-6 ........T.....G..AC.T...........G..G..ACAA.................. 2678

AAV-1 GGCATCGGCAAGACAGGCCAGCAGCCCGCTAAAAAGAGACTCAATTTTGGTCAGACTGGC 2753
AAV-2 ..A.C...A...G.G..........T..A.G...A...T.G.................A 2733
AAV-6 .....T.......................................... 2738

AAV-1 GACTCAGAGTCAGTCCCCGATCCACAACCTCTCGGAGAACCTCCAGCAACCCCCCGCTGCT 2813
AAV-2 ...G....C.....A..T..C..C..G.........C.G..A......G.....T...G. 2793
AAV-6 ...T....G.....C..C..C..A..A.........G.A..T......A.....G..... 2798

                VP3
AAV-1 GTGGGACCTACTACAATGGCTTCAGGCGGTGGCGCACCAATGGCAGACAATAACGAAGGC 2873
AAV-2 C.....A...A...G......A.....A.........................G... 2853
AAV-6 ..... 2858

AAV-1 GCCGACGGAGTGGGTAATGCCTCAGGAAATTGGCATTGCGATTCCACATGGCTGGGCGAC 2933
AAV-2 ..................T....C.............................A........ 2913
AAV-6 ..... 2918

AAV-1 AGAGTCATCACCACCAGCACCCGCACCTGGGCCTTGCCCACCTACAATAACCACCTCTAC 2993
AAV-2 ......................A.........C.............C............ 2973
AAV-6 ......................A..A................T..C............ 2978

AAV-1 AAGCAAATCTCCAGTGCTTCAACGGGGGCCAGCAACGACAACCACTACTTCGGCTACAGC 3053
AAV-2 ..A.....T.....CCAA...---..A...TCG........T........T......... 3030
AAV-6 ..... 3038

AAV-1 ACCCCCTGGGGGTATTTTGATTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGG 3113
AAV-2 .....T..............C..... 3090
AAV-6 ..........T..C..... 3098

AAV-1 CAGCGACTCATCAACAACAATTGGGGATTCCGGCCCAAGAGACTCAACTTCAAACTCTTC 3173
AAV-2 ..AA..............C..........A.....................G.....T 3150
AAV-6 .....G..... 3158

AAV-1 AACATCCAAGTCAAGGAGGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTT 3233
AAV-2 .....T........A.........CA......C..TACG..G..G..T..C......... 3210
AAV-6 .....G..... 3218
```

FIG 1E

```
AAV-1 ACCAGCACGGTTCAAGTCTTCTCGGACTCGGAGTACCAGCTTCCGTACGTCCTCGGCTCT 3293
AAV-2 ..............G..G..TA.T.................C.................G 3270
AAV-6 ..............................T.G..................... 3278

AAV-1 GCGCACCAGGGCTGCCTCCCTCCGTTCCCGGCGGACGTGTTCATGATTCCGCAATACGGC 3353
AAV-2 .....T..A..A........G........A..A.....C......G.G..A..G..T..A 3330
AAV-6 ..................................................G..... 3338

AAV-1 TACCTGACGCTCAACAATGGCAGCCAAGCCGTGGGACGTTCATCCTTTTACTGCCTGGAA 3413
AAV-2 .....C..C..G.....C..G..T..G..A..A.....C..T..A.............G 3390
AAV-6 .....A.....................G..A........G..................... 3398

AAV-1 TATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACTTTACCTTCAGCTACACCTTTGAG 3473
AAV-2 ..C..T..............C.T..C..A.....................T..... 3450
AAV-6 ........A..G.....................T.....................C... 3458

AAV-1 GAAGTGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATCCT 3533
AAV-2 ..C..T.....................T..........T........T..C..... 3510
AAV-6 ..C..................................................... 3498

AAV-1 CTCATCGACCAATACCTGTATTACCTGAACAGAACTCAAAATCAGTCCGGAAGTGCCCAA 3593
AAV-2 ..........G...........T...G.....AA.C.C..CAAGT....CCA..ACG 3570
AAV-6 ..........G.........................G..................... 3578

AAV-1 AACAAGGACTTGCTGTTTAGCCGTGGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAAC 3653
AAV-2 C.GTCAAGGC.T.A....TCT.AG.CCGGAG.GAG..A...TCGG.AC...T.T.GG... 3630
AAV-6 ......................G..................................... 3638

AAV-1 TGGCTACCTGGACCCTGTTATCGGCAGCAGCGCGTTTCTAAAACAAAAACAGACAACAAC 3713
AAV-2 .....T.............C..C........A..A.CA..G...TCTG.G..T..... 3690
AAV-6 ....................C..................................... 3698

AAV-1 AACAGCAATTTTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGGCGTGAATCCATC 3773
AAV-2 .....TG.A.ACT.G........A...A.C..G..CC..........CA.A..C..TC.G 3750
AAV-6 ........C.............................T.............T..A 3758

AAV-1 ATCAACCCTGGCACTGCTATGGCCTCACACAAAGACGACGAAGACAAGTTCTTTCCCATG 3833
AAV-2 G.G..T..G..GC.C..C.....AAGC.....G.....T.....A.....T.....TCA. 3810
AAV-6 ..................................A..................... 3818

AAV-1 AGCGGTGTCATGATTTTTGGAAAAGAGAGCGCCGGAGCTTCAAACACTGCATTGGACAAT 3893
AAV-2 .....G..TC.C..C.....G..GC.AG..T.A.AGAAAA....TGTGAACA.T..A..G 3870
AAV-6 ........................G..................................... 3878

AAV-1 GTCATGATTACAGACGAAGAGGAAATTAAAGCCACTAACCCTGTGGCCACCGAAAGATTT 3953
AAV-2 ............................CGG.A.A..C..T..C.....T..G..GCAG.A. 3930
AAV-6 ........C..................C..............C.................. 3938

AAV-1 GGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCCTGCGACCGGAGATGTGCAT 4013
AAV-2 ..TT.T..AT.TAC...CC.......AG...A..G.C.AG.A..T....C......CA.C 3990
AAV-6 .....T............C..................................... 3998

AAV-1 GCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTGCAGGGTCCC 4073
AAV-2 A.ACAA..C.TTC.T..A........C.....G..C.....T........T.....G... 4050
AAV-6 T..........C........A..............C........A..............T 4058
```

FIG 1F

```
AAV-1 ATTTGGGCCAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGC 4133
AAV-2 ..C.....A..G.....A.....G..C.....T........C.....C..C.....T..A 4110
AAV-6 ......................G.............................C......... 4118

AAV-1 TTTGGACTCAAGAACCCGCCTCCTCAGATCCTCATCAAAAACACGCCTGTTCCTGCGAAT 4193
AAV-2 ..C.....T..AC....T.....A.....T........G.....C..G..A......... 4170
AAV-6 ........T...C.......................................... 4178

AAV-1 CCTCCGGCGGAGTTTTCAGCTACAAAGTTTGCTTCATTCATCACCCAATACTCCACAGGA 4253
AAV-2 ...T..A.CACC..CAGT..GG.............C.........A..G.........G... 4230
AAV-6 ........A........G.............................G..T......... 4238

AAV-1 CA-AGTGAGTGTGGAAATTGAATGGGAGCTGCAGAAAGAAAACAGCAAGCGCTGGAATCC 4312
AAV-2 ..CG..C..C.....G..C..G.............G...........A.......... 4290
AAV-6 ..-.......C.....G.............................A.......... 4297

AAV-1 CGAAGTGCAGTACACATCCAATTATGCAAAATCTGCCAA-CGTTGATTTTACTGTGGACA 4371
AAV-2 ....A.T........T.....C..CAAC..G....TT..T...G..C.....C.....T. 4350
AAV-6 ............T.....T..C...............-.........C.......... 4356

AAV-1 ACAATGGACTTTATACTGAGCCTCGCCCCATTGGCACCCGTTACCTTACCCGTCCCCTGT 4431
AAV-2 CT.....CG.G...T.A.......................A.A.....G..T...AAT.... 4410
AAV-6 ..................................C.............. 4416

      VP1-3 stop   PolyA signal
AAV-1 AATTACGTGTTAATCAATAAACCGGTTGATTCGTTTCAGTTGAACTTTGGTCTCCTGTCC 4491
AAV-2 ....G.T..................T..A.........................TGCGTA 4470
AAV-6 ....GT.....................A.....G.....................A....G 4476

AAV-1 TTCTTATCTTATC-GGTTACCATGGTTAT-AGCTTACACATTA--ACTGCTTGGTTGCGC 4547
AAV-2 ..TC.T.......TA...T......C..CGTAGA..AGT.GC.TGG.G.G..AA.CATTA 4530
AAV-6 ..A..........T...C.....A.CA.C-C.G..........--.......A....... 4533

AAV-1 TTCGCGATAAAAGACTTACGTCATCGGGttacccctagtgatggagttgcccactccctc 4607
AAV-2 ACTA.A.gg.a--------------------.....................g.......... 4570
AAV-6 .......at.--------------------.............................. 4572

AAV-1 tctgcgcgctcgctcgctcggtggggccggcagagcagagctctgccgtctgcggacctt 4667
AAV-2 .c.................ac..a......gc..c..a..g..gc...a.gc.c.gg... 4630
AAV-6 .a.....................g.............................. 4632

AAV-1 tggtccgcaggccccaccgagcgagcgagcgcgcagagagggagtgggcaa          4718
AAV-2 ..cc.g.gc....t..gt.............................c...          4681
AAV-6 ..................................t.............              4683
```

09/807802
PCT/US99/25694

AAV-1 TR

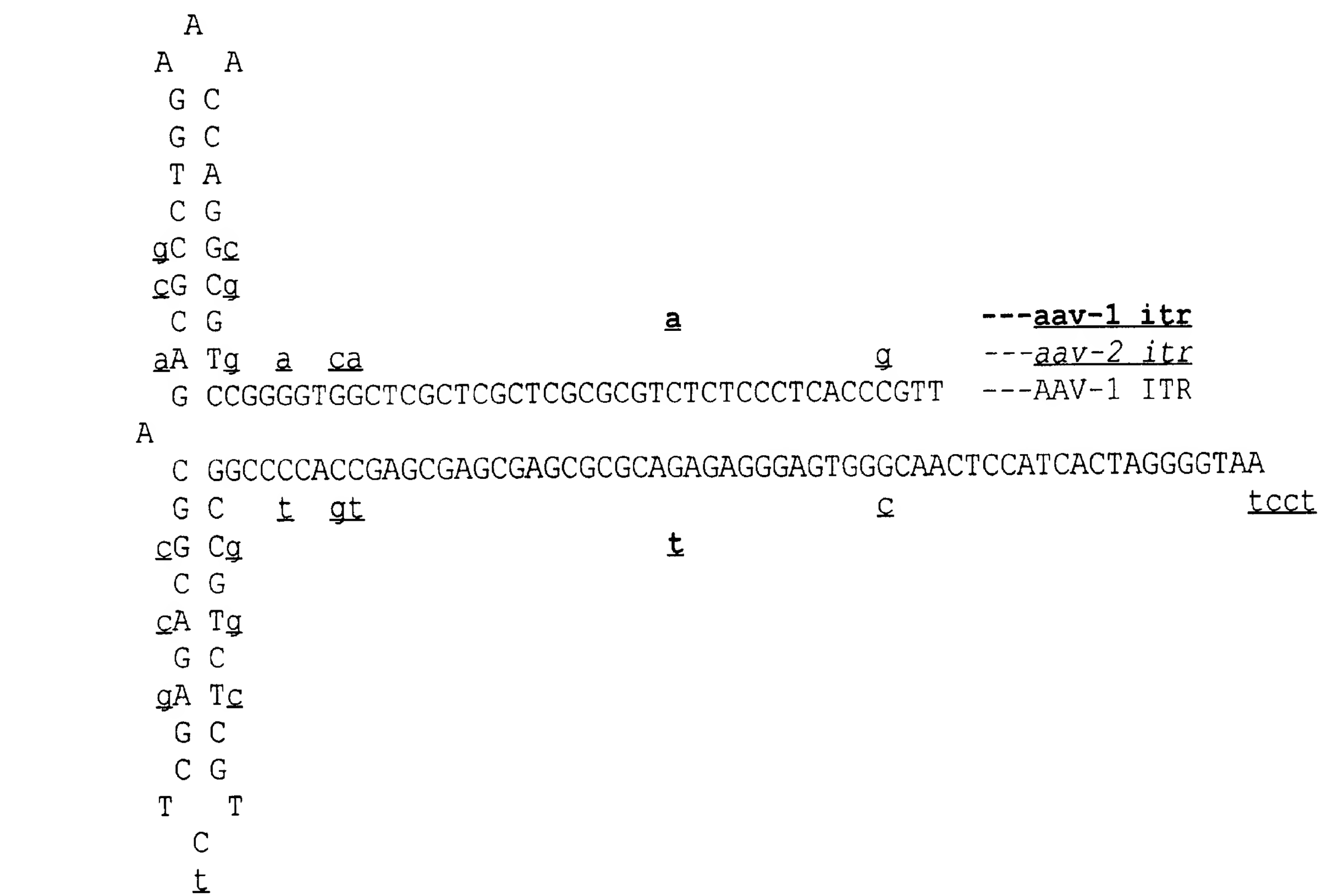


FIG 2

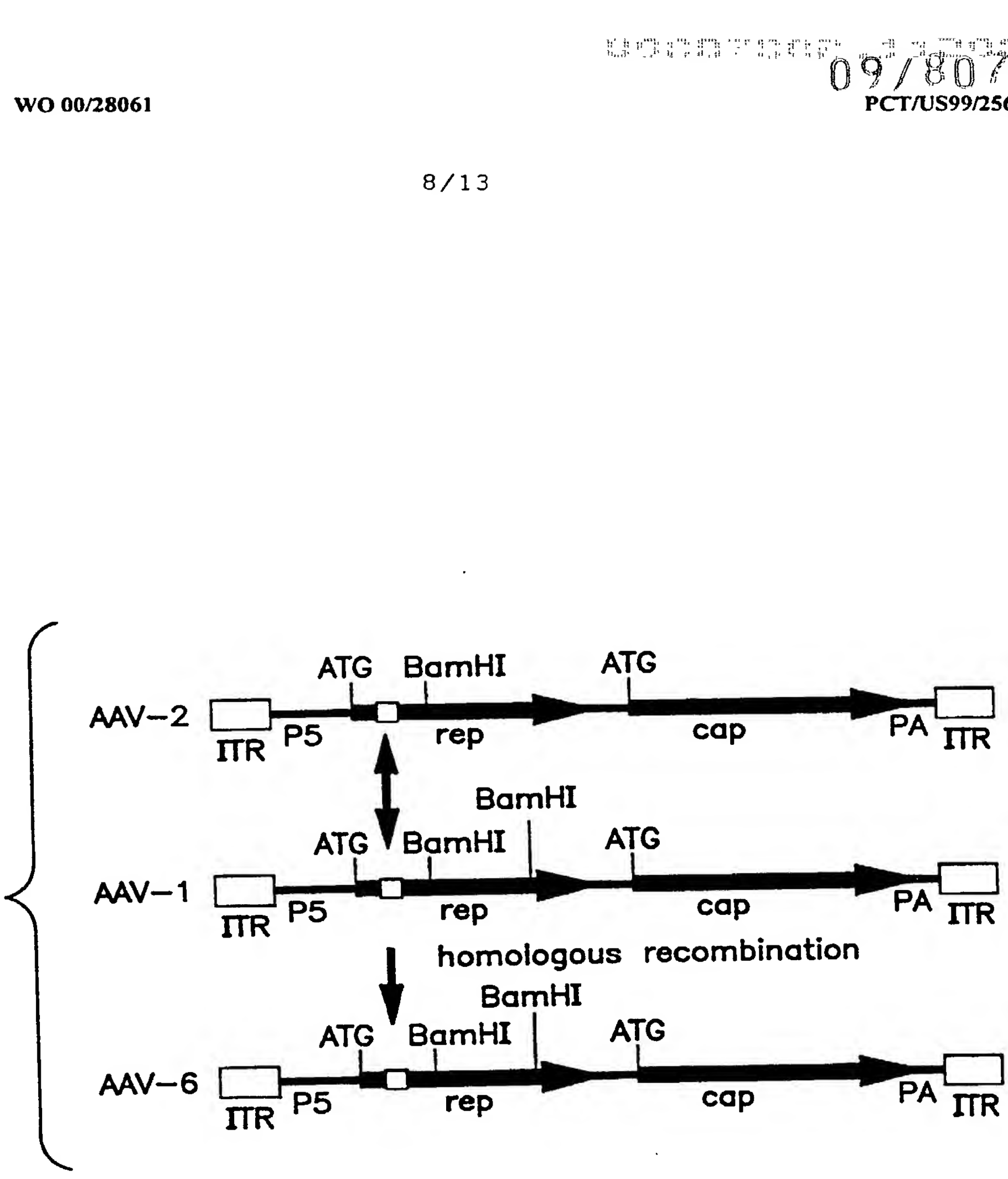

AAV-2
ITR
P5
ATG
BamHI
rep
ATG
cap
PA
ITR
AAV-1
BamHI
ATG
BamHI
rep
ATG
cap
PA
ITR
homologous recombination
AAV-6
BamHI
ATG
BamHI
rep
ATG
cap
PA
ITR

FIG. 3A

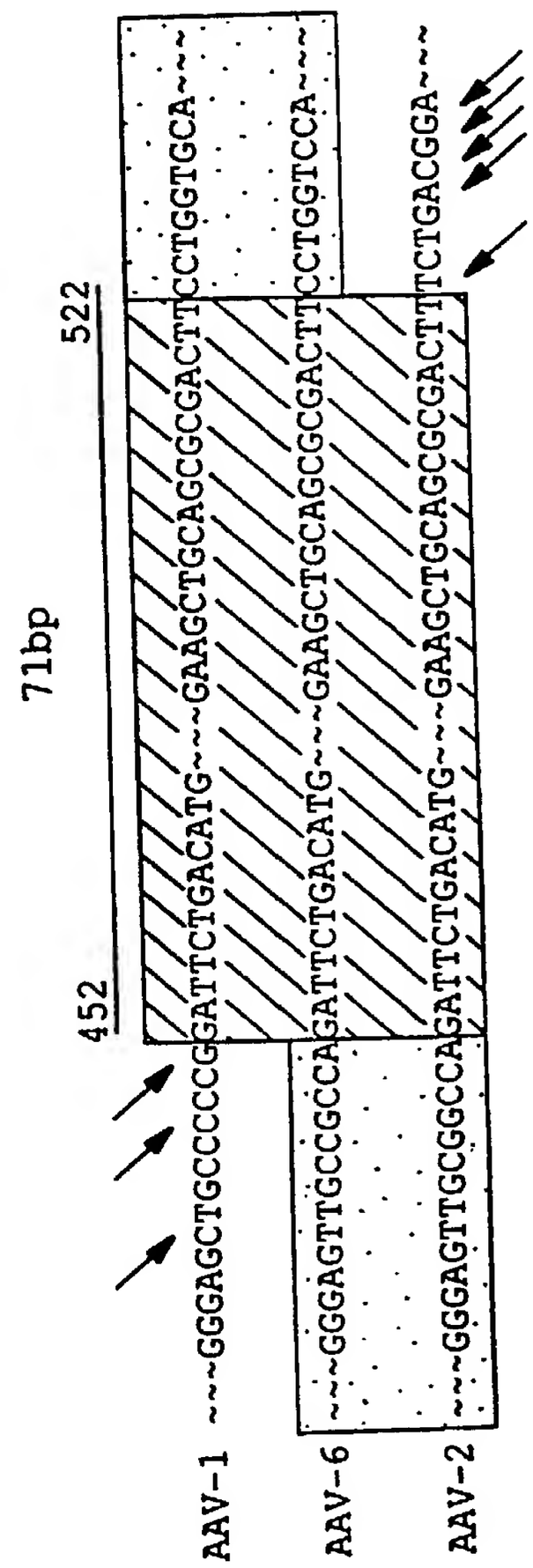

71bp
522
452
AAV-1 ~~~GGGAGCTGCCCCCGGGATTCTGACATG~~~GAAGCTGCAGCGCGACTTCCTGGTGCA~~~
AAV-6 ~~~GGGAGTTGCCGCCAGATTCTGACATG~~~GAAGCTGCAGCGCGACTTCCTGGTCCA~~~
AAV-2 ~~~GGGAGTTGCGGCCAGATTCTGACATG~~~GAAGCTGCAGCGCGACTTTCTGACGGA~~~

FIG. 3B

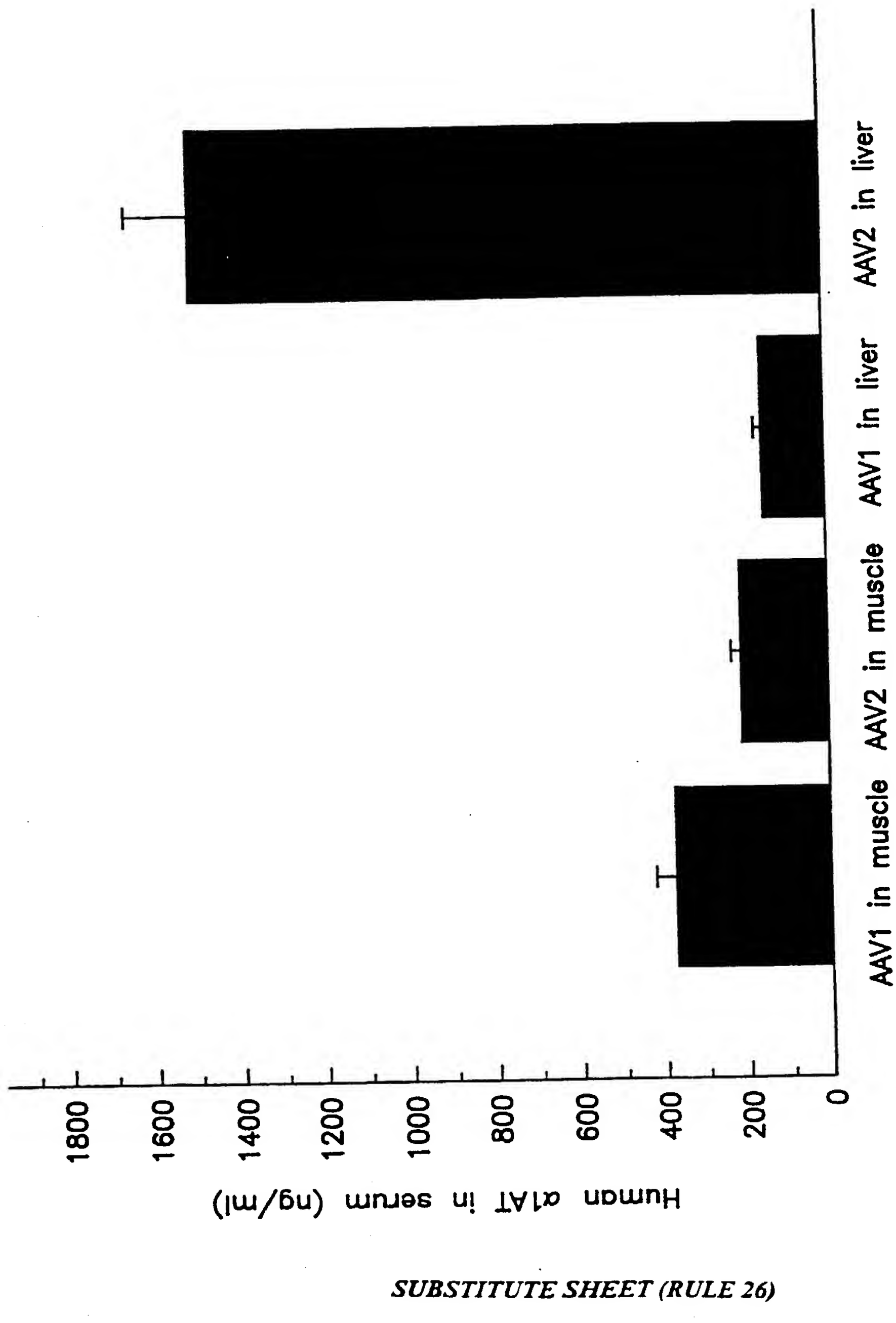

Human α1AT in serum (ng/ml)
0
200
400
600
800
1000
1200
1400
1600
1800
AAV1 in muscle
AAV1 in liver
AAV2 in muscle
AAV2 in liver

FIG. 4A

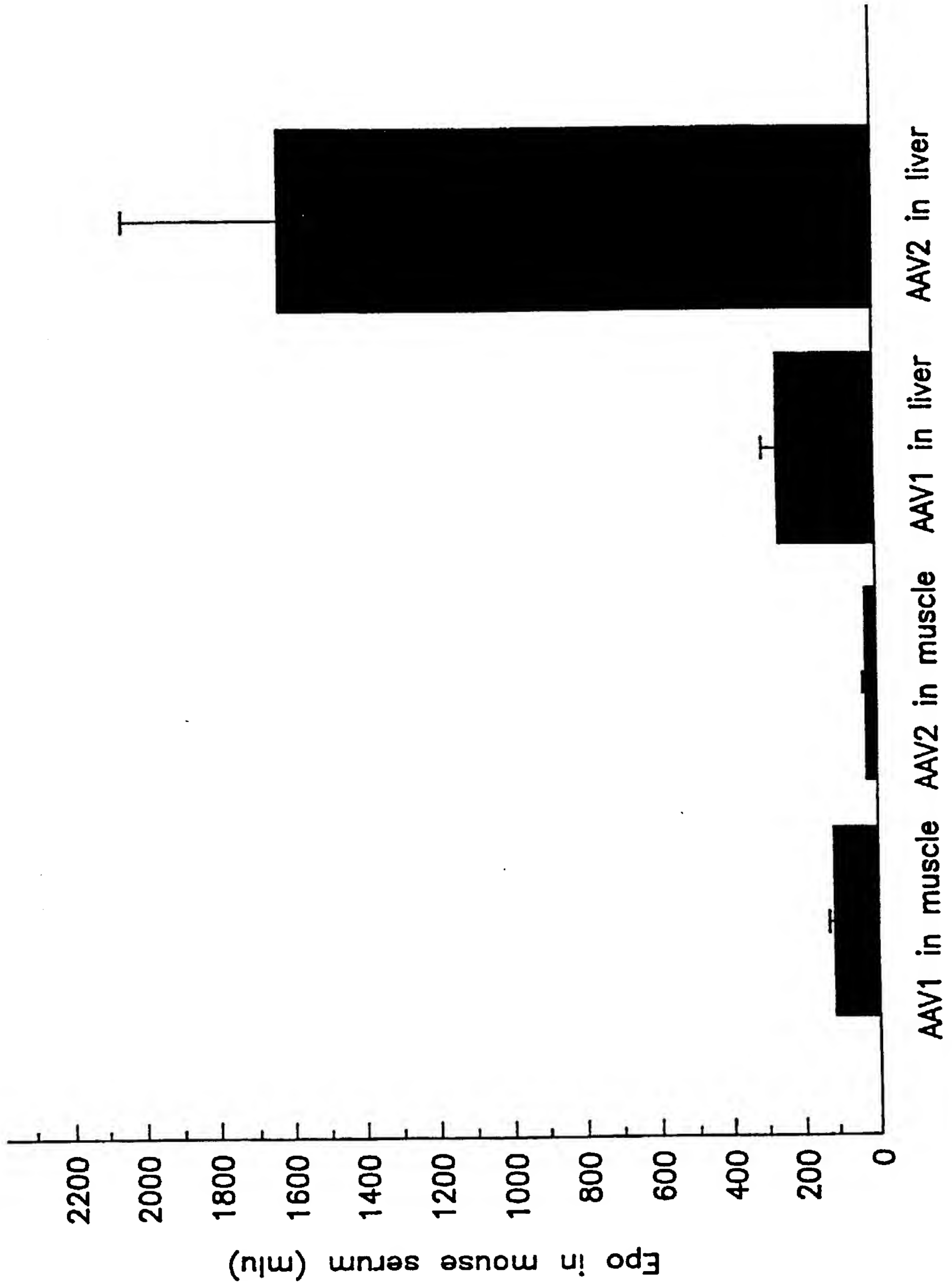

Epo in mouse serum (mIu)
2200
2000
1800
1600
1400
1200
1000
800
600
400
200
0
AAV1 in muscle
AAV2 in liver
AAV1 in liver
AAV2 in muscle

FIG. 4B

FIG. 5A

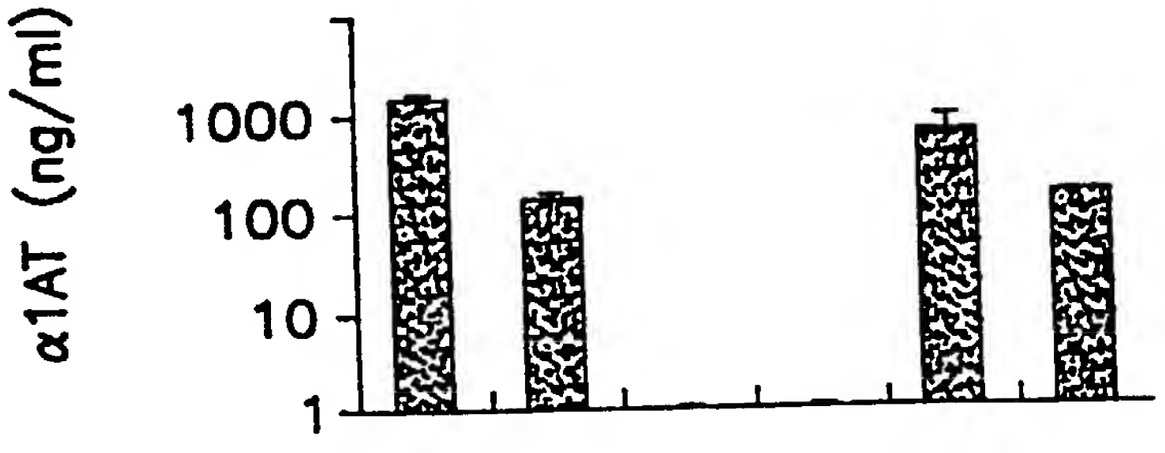


FIG. 5B

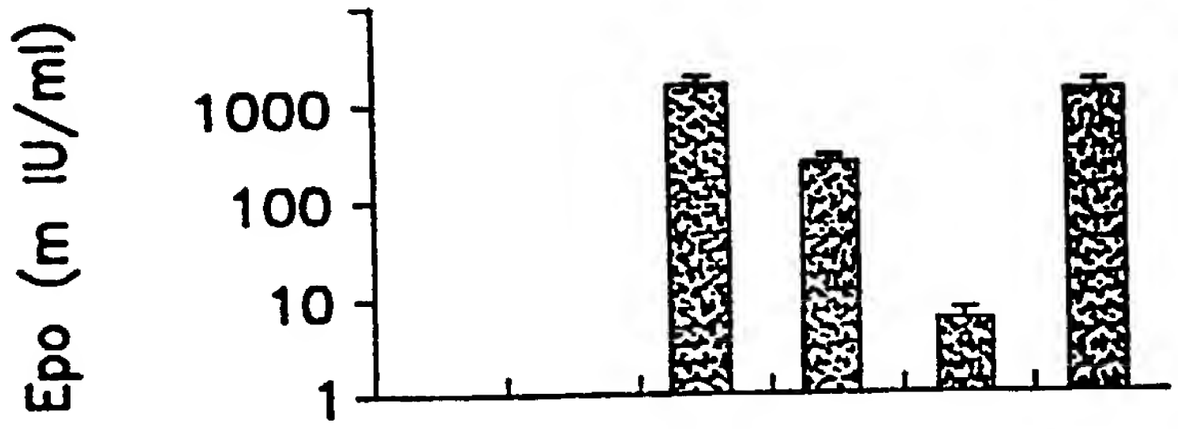


FIG. 5C

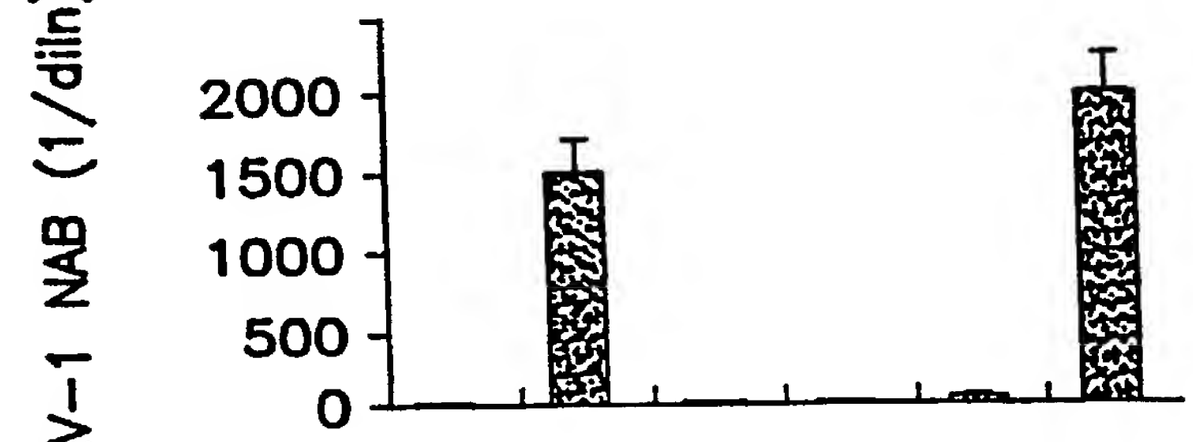
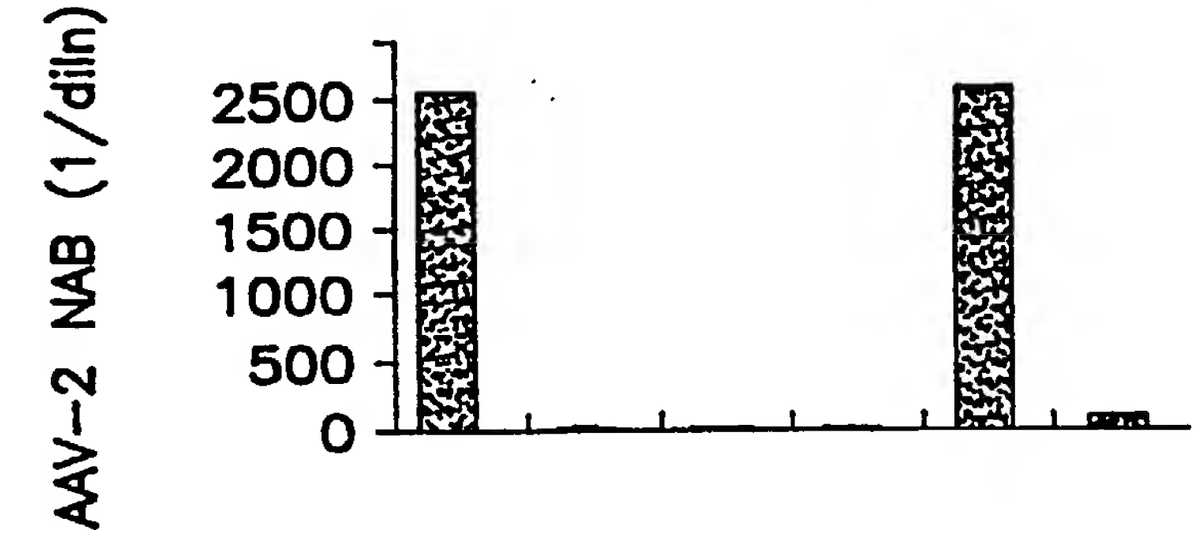


FIG. 5D



Group	1	2	3	4	5	6
Vector1– α1AT	AAV2	AAV1	PBS	PBS	AAV2	AAV1
Vector2–EPO	AAV2	AAV1	AAV2	AAV1	AAV1	AAV2

FIG. 6A

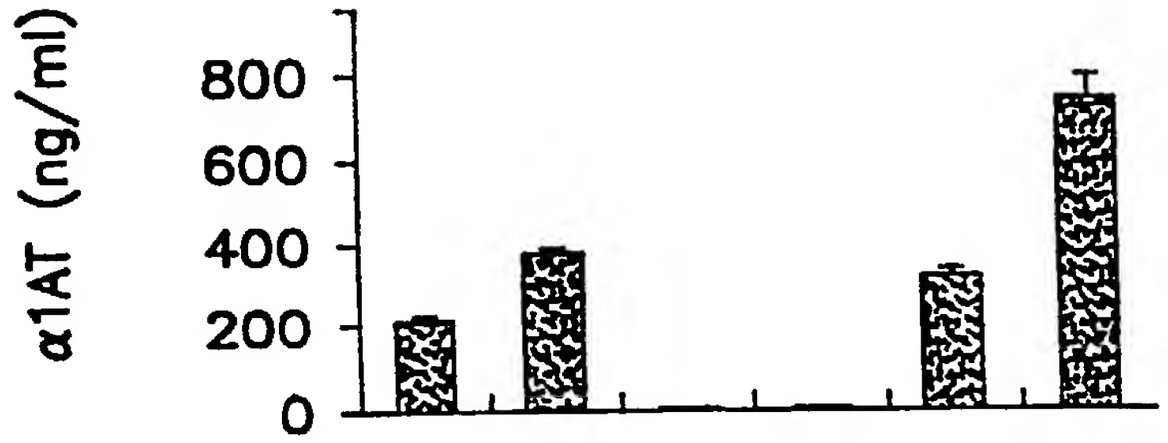


FIG. 6B

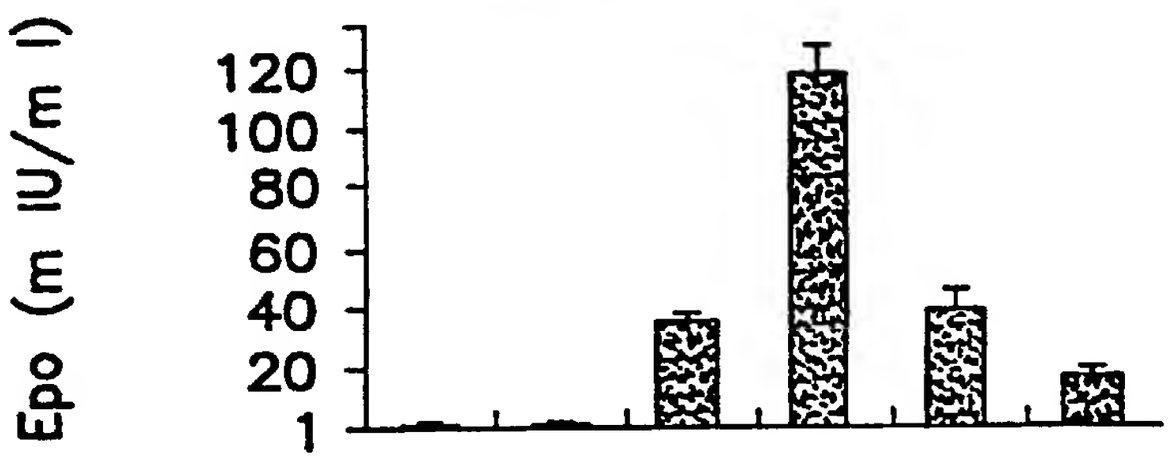


FIG. 6C

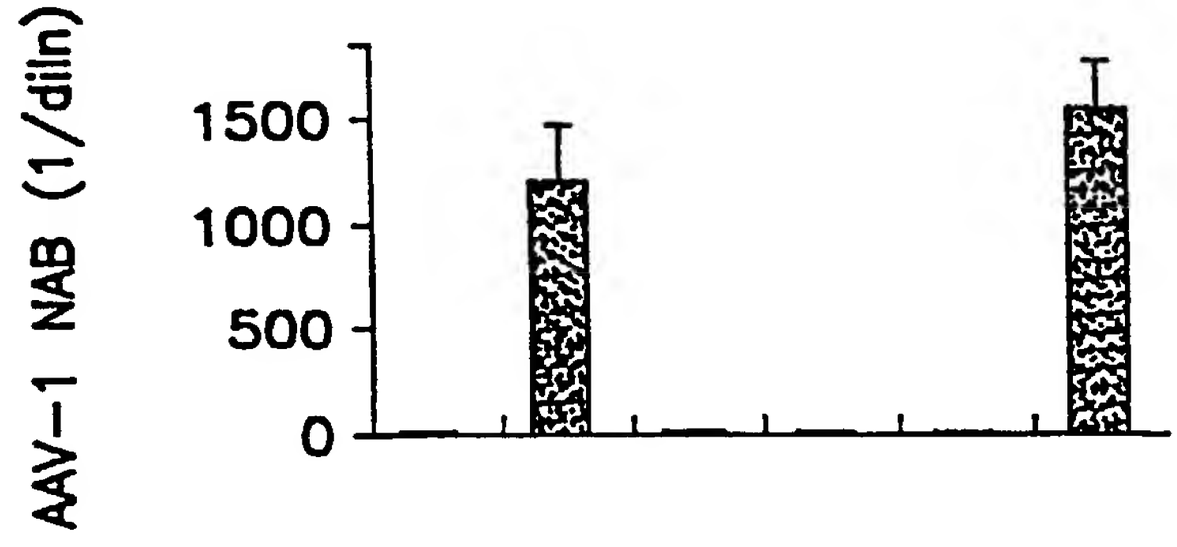
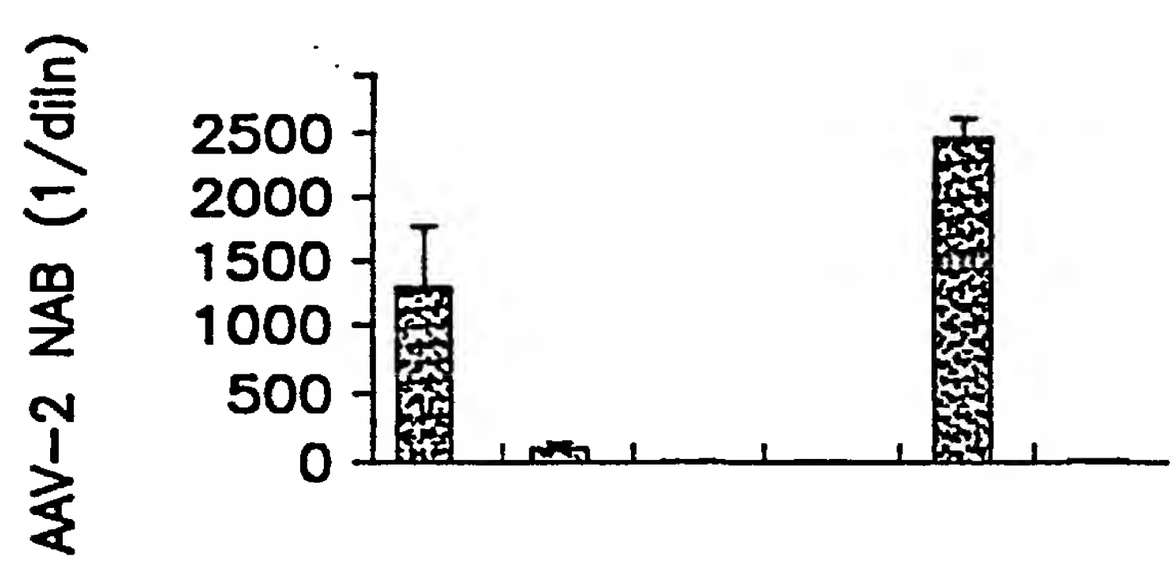


FIG. 6D



Group	1	2	3	4	5	6
Vector1 – α1AT	AAV2	AAV1	PBS	PBS	AAV2	AAV1
Vector2–EPO	AAV2	AAV1	AAV2	AAV1	AAV1	AAV2

DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled ADENO-ASSOCIATED VIRUS SEROTYPE I NUCLEIC ACID SEQUENCES, VECTORS AND HOST CELLS CONTAINING SAME, the specification of which

(check one)
- ___ is attached hereto
- X was filed on April 17, 2001 as Application No. 09/807,802 and was amended on April 17, 2001. (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR 1.56, including for continuation-in-part applications, material information which became available between the filing date of the prior application and the national or PCT international filing date of the continuation-in-part application.

I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT international application which designated at least one country other than the United States of America, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or any PCT international application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)			Priority Not Claimed	Certified Copy Attached?	
(Number)	(Country)	(MM/DD/YYYY)		Yes	No

I hereby claim the benefit under 35 U.S.C. 119(e) of any United States provisional application(s) listed below.

(Application Number)	(Filing Date, MM/DD/YYYY)
60/107,114	November 5, 1998

I hereby appoint the following attorneys and agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: STANLEY B. KITA, Registration No. 24,561; GEORGE A. SMITH, JR., Registration No. 24,442; MARY E. BAK, Registration No. 31,215, CATHY A. KODROFF, Registration Number 33,980, WILLIAM BAK, Registration Number 37,277, HENRY HANSEN, Registration No. 19,612, and TRACY U. PALOVICH, Registration No. 47,840.

Address all telephone calls to Cathy A. Kodroff at telephone no. (215) 540-9210. Address all correspondence to HOWSON AND HOWSON, Spring House Corporate Center, P. O. Box 457, Spring House, Pennsylvania 19477.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of first inventor: James M. Wilson

Inventor's signature _____ _____
Date

Residence: Gladwyne, Pennsylvania 19035
Citizenship: United States of America
Post Office Address: 1350 N. Avignon Drive, Gladwyne, Pennsylvania 19035

2-02

Full name of first inventor: Weidong Xiao

Inventor's signature Weidong Xiao 11/27/01
Date

Residence: Fort Washington, Pennsylvania 19034
Citizenship: China CNX
Post Office Address: 1604 Conquest Way, Fort Washington, Pennsylvania 19034

I hereby appoint the following attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: STANLEY B. KITA, Registration No. 24,561; GEORGE A. SMITH, JR., Registration No. 24,442; WILSON OBERDORFER, Registration No. 17,379; MARY E. BAK, Registration No. 31,215, CATHY A. KODROFF, Registration Number 33,980, HENRY HANSEN, Registration No. 19,612, and WILLIAM BAK, Registration Number 37,277.

Address all telephone calls to Cathy A. Kodroff at telephone no. (215) 540-9210. Address all correspondence to HOWSON AND HOWSON, Spring House Corporate Center, P. O. Box 457, Spring House, Pennsylvania 19477.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under 18 U.S.C. 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full name of first inventor: James M. Wilson

Inventor's signature _____ 3-16-01
Date

Residence: Gladwyne, Pennsylvania 19035
Citizenship: United States of America USX
Post Office Address: 1350 N. Avignon Drive, Gladwyne, Pennsylvania 19035

Full name of first inventor: Weidong Xiao

Inventor's signature _____ _____
Date

Residence: Jenkintown, Pennsylvania 19046
Citizenship: China
Post Office Address: 155 Washington Lane, Apt. P4, Jenkintown, Pennsylvania 19046

SEQUENCE LISTING

<110> Wilson, James M.
Xiao, Weidong
The Trustees of the University of Pennsylvania

<120> Adeno-Associated Virus Serotype I Nucleic Acid Sequences, Vectors and Host Cells Containing Same

<130> GNVPN.031PCT

<140>
<141>

<150> 60/107,114
<151> 1998-11-05

<160> 20

<170> PatentIn Ver. 2.0

<210> 1
<211> 4718
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (335)..(2206)

<220>
<221> CDS
<222> (2223)..(4430)

<400> 1

ttgcccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcag agagggagtg 120

ggcaactcca tcactagggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180

cgtaaattac gtcatagggg agtggtcctg tattagctgt cacgtgagtg cttttgcgac 240

attttgcgac accacgtggc catttagggt atatatggcc gagtgagcga gcaggatctc 300

cattttgacc gcgaaatttg aacgagcagc agcc atg ccg ggc ttc tac gag atc 355
Met Pro Gly Phe Tyr Glu Ile
1 5

```
gtg atc aag gtg ccg agc gac ctg gac gag cac ctg ccg ggc att tct   403
Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser
         10                  15                  20

gac tcg ttt gtg agc tgg gtg gcc gag aag gaa tgg gag ctg ccc ccg   451
Asp Ser Phe Val Ser Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro
     25                  30                  35

gat tct gac atg gat ctg aat ctg att gag cag gca ccc ctg acc gtg   499
Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val
 40                  45                  50                  55

gcc gag aag ctg cag cgc gac ttc ctg gtc caa tgg cgc cgc gtg agt   547
Ala Glu Lys Leu Gln Arg Asp Phe Leu Val Gln Trp Arg Arg Val Ser
                 60                  65                  70

aag gcc ccg gag gcc ctc ttc ttt gtt cag ttc gag aag ggc gag tcc   595
Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser
             75                  80                  85

tac ttc cac ctc cat att ctg gtg gag acc acg ggg gtc aaa tcc atg   643
Tyr Phe His Leu His Ile Leu Val Glu Thr Thr Gly Val Lys Ser Met
         90                  95                  100

gtg ctg ggc cgc ttc ctg agt cag att agg gac aag ctg gtg cag acc   691
Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Asp Lys Leu Val Gln Thr
     105                 110                 115

atc tac cgc ggg atc gag ccg acc ctg ccc aac tgg ttc gcg gtg acc   739
Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr
120                 125                 130                 135

aag acg cgt aat ggc gcc gga ggg ggg aac aag gtg gtg gac gag tgc   787
Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys
                140                 145                 150

tac atc ccc aac tac ctc ctg ccc aag act cag ccc gag ctg cag tgg   835
Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp
            155                 160                 165

gcg tgg act aac atg gag gag tat ata agc gcc tgt ttg aac ctg gcc   883
Ala Trp Thr Asn Met Glu Glu Tyr Ile Ser Ala Cys Leu Asn Leu Ala
        170                 175                 180

gag cgc aaa cgg ctc gtg gcg cag cac ctg acc cac gtc agc cag acc   931
Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr
    185                 190                 195
```

```
cag gag cag aac aag gag aat ctg aac ccc aat tct gac gcg cct gtc    979
Gln Glu Gln Asn Lys Glu Asn Leu Asn Pro Asn Ser Asp Ala Pro Val
200                 205                 210                 215

atc cgg tca aaa acc tcc gcg cgc tac atg gag ctg gtc ggg tgg ctg    1027
Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu
                220                 225                 230

gtg gac cgg ggc atc acc tcc gag aag cag tgg atc cag gag gac cag    1075
Val Asp Arg Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln
            235                 240                 245

gcc tcg tac atc tcc ttc aac gcc gct tcc aac tcg cgg tcc cag atc    1123
Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile
        250                 255                 260

aag gcc gct ctg gac aat gcc ggc aag atc atg gcg ctg acc aaa tcc    1171
Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ala Leu Thr Lys Ser
    265                 270                 275

gcg ccc gac tac ctg gta ggc ccc gct ccg ccc gcg gac att aaa acc    1219
Ala Pro Asp Tyr Leu Val Gly Pro Ala Pro Pro Ala Asp Ile Lys Thr
280                 285                 290                 295

aac cgc atc tac cgc atc ctg gag ctg aac ggc tac gaa cct gcc tac    1267
Asn Arg Ile Tyr Arg Ile Leu Glu Leu Asn Gly Tyr Glu Pro Ala Tyr
                300                 305                 310

gcc ggc tcc gtc ttt ctc ggc tgg gcc cag aaa agg ttc ggg aag cgc    1315
Ala Gly Ser Val Phe Leu Gly Trp Ala Gln Lys Arg Phe Gly Lys Arg
            315                 320                 325

aac acc atc tgg ctg ttt ggg ccg gcc acc acg ggc aag acc aac atc    1363
Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile
        330                 335                 340

gcg gaa gcc atc gcc cac gcc gtg ccc ttc tac ggc tgc gtc aac tgg    1411
Ala Glu Ala Ile Ala His Ala Val Pro Phe Tyr Gly Cys Val Asn Trp
    345                 350                 355

acc aat gag aac ttt ccc ttc aat gat tgc gtc gac aag atg gtg atc    1459
Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile
360                 365                 370                 375

tgg tgg gag gag ggc aag atg acg gcc aag gtc gtg gag tcc gcc aag    1507
Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys
                380                 385                 390
```

```
gcc att ctc ggc ggc agc aag gtg cgc gtg gac caa aag tgc aag tcg   1555
Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser
            395                 400                 405

tcc gcc cag atc gac ccc acc ccc gtg atc gtc acc tcc aac acc aac   1603
Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn
        410                 415                 420

atg tgc gcc gtg att gac ggg aac agc acc acc ttc gag cac cag cag   1651
Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln
    425                 430                 435

ccg ttg cag gac cgg atg ttc aaa ttt gaa ctc acc cgc cgt ctg gag   1699
Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Glu
440                 445                 450                 455

cat gac ttt ggc aag gtg aca aag cag gaa gtc aaa gag ttc ttc cgc   1747
His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Glu Phe Phe Arg
                460                 465                 470

tgg gcg cag gat cac gtg acc gag gtg gcg cat gag ttc tac gtc aga   1795
Trp Ala Gln Asp His Val Thr Glu Val Ala His Glu Phe Tyr Val Arg
            475                 480                 485

aag ggt gga gcc aac aaa aga ccc gcc ccc gat gac gcg gat aaa agc   1843
Lys Gly Gly Ala Asn Lys Arg Pro Ala Pro Asp Asp Ala Asp Lys Ser
        490                 495                 500

gag ccc aag cgg gcc tgc ccc tca gtc gcg gat cca tcg acg tca gac   1891
Glu Pro Lys Arg Ala Cys Pro Ser Val Ala Asp Pro Ser Thr Ser Asp
    505                 510                 515

gcg gaa gga gct ccg gtg gac ttt gcc gac agg tac caa aac aaa tgt   1939
Ala Glu Gly Ala Pro Val Asp Phe Ala Asp Arg Tyr Gln Asn Lys Cys
520                 525                 530                 535

tct cgt cac gcg ggc atg ctt cag atg ctg ttt ccc tgc aag aca tgc   1987
Ser Arg His Ala Gly Met Leu Gln Met Leu Phe Pro Cys Lys Thr Cys
                540                 545                 550

gag aga atg aat cag aat ttc aac att tgc ttc acg cac ggg acg aga   2035
Glu Arg Met Asn Gln Asn Phe Asn Ile Cys Phe Thr His Gly Thr Arg
            555                 560                 565

gac tgt tca gag tgc ttc ccc ggc gtg tca gaa tct caa ccg gtc gtc   2083
Asp Cys Ser Glu Cys Phe Pro Gly Val Ser Glu Ser Gln Pro Val Val
        570                 575                 580
```

```
aga aag agg acg tat cgg aaa ctc tgt gcc att cat cat ctg ctg ggg   2131
Arg Lys Arg Thr Tyr Arg Lys Leu Cys Ala Ile His His Leu Leu Gly
    585                 590                 595

cgg gct ccc gag att gct tgc tcg gcc tgc gat ctg gtc aac gtg gac   2179
Arg Ala Pro Glu Ile Ala Cys Ser Ala Cys Asp Leu Val Asn Val Asp
600                 605                 610                 615

ctg gat gac tgt gtt tct gag caa taa atgacttaaa ccaggt atg gct gcc 2231
Leu Asp Asp Cys Val Ser Glu Gln                     Met Ala Ala
                620                                 625

gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct gag ggc att   2279
Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile
        630                 635                 640

cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc aaa gcc aac   2327
Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn
    645                 650                 655

cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct ggc tac aag   2375
Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys
660                 665                 670                 675

tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc gtc aac gcg   2423
Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala
                680                 685                 690

gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac cag cag ctc   2471
Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu
            695                 700                 705

aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc gac gcc gag   2519
Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu
        710                 715                 720

ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc aac ctc ggg   2567
Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly
    725                 730                 735

cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct ctc ggt ctg   2615
Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu
740                 745                 750                 755

gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt ccg gta gag   2663
Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Val Glu
                760                 765                 770
```

```
cag tcg cca caa gag cca gac tcc tcc tcg ggc atc ggc aag aca ggc   2711
Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly
            775                 780                 785

cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act ggc gac tca   2759
Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser
        790                 795                 800

gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca gca acc ccc   2807
Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro
    805                 810                 815

gct gct gtg gga cct act aca atg gct tca ggc ggt ggc gca cca atg   2855
Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly Ala Pro Met
820                 825                 830                 835

gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc tca gga aat   2903
Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn
                840                 845                 850

tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc acc acc agc   2951
Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser
            855                 860                 865

acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc tac aag caa   2999
Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln
        870                 875                 880

atc tcc agt gct tca acg ggg gcc agc aac gac aac cac tac ttc ggc   3047
Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His Tyr Phe Gly
    885                 890                 895

tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc cac tgc cac   3095
Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
900                 905                 910                 915

ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat tgg gga ttc   3143
Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
                920                 925                 930

cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa gtc aag gag   3191
Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
            935                 940                 945

gtc acg acg aat gat ggc gtc aca acc atc gct aat aac ctt acc agc   3239
Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser
        950                 955                 960
```

```
acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg tac gtc ctc   3287
Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
    965                 970                 975

ggc tct gcg cac cag ggc tgc ctc cct ccg ttc ccg gcg gac gtg ttc   3335
Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
980                 985                 990                 995

atg att ccg caa tac ggc tac ctg acg ctc aac aat ggc agc caa gcc   3383
Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala
                1000                1005                1010

gtg gga cgt tca tcc ttt tac tgc ctg gaa tat ttc cct tct cag atg   3431
Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met
            1015                1020                1025

ctg aga acg ggc aac aac ttt acc ttc agc tac acc ttt gag gaa gtg   3479
Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val
        1030                1035                1040

cct ttc cac agc agc tac gcg cac agc cag agc ctg gac cgg ctg atg   3527
Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met
    1045                1050                1055

aat cct ctc atc gac caa tac ctg tat tac ctg aac aga act caa aat   3575
Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn
1060                1065                1070                1075

cag tcc gga agt gcc caa aac aag gac ttg ctg ttt agc cgt ggg tct   3623
Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser
                1080                1085                1090

cca gct ggc atg tct gtt cag ccc aaa aac tgg cta cct gga ccc tgt   3671
Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys
            1095                1100                1105

tat cgg cag cag cgc gtt tct aaa aca aaa aca gac aac aac aac agc   3719
Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser
        1110                1115                1120

aat ttt acc tgg act ggt gct tca aaa tat aac ctc aat ggg cgt gaa   3767
Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu
    1125                1130                1135

tcc atc atc aac cct ggc act gct atg gcc tca cac aaa gac gac gaa   3815
Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys Asp Asp Glu
1140                1145                1150                1155
```

```
gac aag ttc ttt ccc atg agc ggt gtc atg att ttt gga aaa gag agc   3863
Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly Lys Glu Ser
                1160                1165                1170

gcc gga gct tca aac act gca ttg gac aat gtc atg att aca gac gaa   3911
Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile Thr Asp Glu
            1175                1180                1185

gag gaa att aaa gcc act aac cct gtg gcc acc gaa aga ttt ggg acc   3959
Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg Phe Gly Thr
        1190                1195                1200

gtg gca gtc aat ttc cag agc agc agc aca gac cct gcg acc gga gat   4007
Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp
    1205                1210                1215

gtg cat gct atg gga gca tta cct ggc atg gtg tgg caa gat aga gac   4055
Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
1220                1225                1230                1235

gtg tac ctg cag ggt ccc att tgg gcc aaa att cct cac aca gat gga   4103
Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly
                1240                1245                1250

cac ttt cac ccg tct cct ctt atg ggc ggc ttt gga ctc aag aac ccg   4151
His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys Asn Pro
            1255                1260                1265

cct cct cag atc ctc atc aaa aac acg cct gtt cct gcg aat cct ccg   4199
Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
        1270                1275                1280

gcg gag ttt tca gct aca aag ttt gct tca ttc atc acc caa tac tcc   4247
Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
    1285                1290                1295

aca gga caa gtg agt gtg gaa att gaa tgg gag ctg cag aaa gaa aac   4295
Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn
1300                1305                1310                1315

agc aag cgc tgg aat ccc gaa gtg cag tac aca tcc aat tat gca aaa   4343
Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys
                1320                1325                1330

tct gcc aac gtt gat ttt act gtg gac aac aat gga ctt tat act gag   4391
Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu
            1335                1340                1345
```

```
cct cgc ccc att ggc acc cgt tac ctt acc cgt ccc ctg taattacgtg    4440
Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
      1350                1355                1360

ttaatcaata aaccggttga ttcgtttcag ttgaactttg gtctcctgtc cttcttatct 4500

tatcggttac catggttata gcttacacat taactgcttg gttgcgcttc gcgataaaag 4560

acttacgtca tcgggttacc cctagtgatg gagttgccca ctccctctct gcgcgctcgc 4620

tcgctcggtg gggcctgcgg accaaaggtc cgcagacggc agagctctgc tctgccggcc 4680

ccaccgagcg agcgagcgcg cagagaggga gtgggcaa                          4718
```

<210> 2
<211> 623
<212> PRT
<213> AAV-1

<400> 2

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
 1               5                  10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140
```

```
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400
```

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 3
<211> 736
<212> PRT
<213> AAV-1

<400> 3

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
  1               5                  10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
             20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
         35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
     50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                 85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn

500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 4
<211> 1872
<212> DNA

<213> AAV-1

<220>
<221> CDS
<222> (1)..(1869)

<400> 4

```
atg ccg ggc ttc tac gag atc gtg atc aag gtg ccg agc gac ctg gac    48
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1               5                  10                  15

gag cac ctg ccg ggc att tct gac tcg ttt gtg agc tgg gtg gcc gag    96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ctg ccc ccg gat tct gac atg gat ctg aat ctg att   144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttc ctg   192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

gtc caa tgg cgc cgc gtg agt aag gcc ccg gag gcc ctc ttc ttt gtt   240
Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

cag ttc gag aag ggc gag tcc tac ttc cac ctc cat att ctg gtg gag   288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

acc acg ggg gtc aaa tcc atg gtg ctg ggc cgc ttc ctg agt cag att   336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

agg gac aag ctg gtg cag acc atc tac cgc ggg atc gag ccg acc ctg   384
Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

ccc aac tgg ttc gcg gtg acc aag acg cgt aat ggc gcc gga ggg ggg   432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

aac aag gtg gtg gac gag tgc tac atc ccc aac tac ctc ctg ccc aag   480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

act cag ccc gag ctg cag tgg gcg tgg act aac atg gag gag tat ata   528
```

```
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

agc gcc tgt ttg aac ctg gcc gag cgc aaa cgg ctc gtg gcg cag cac   576
Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acc cac gtc agc cag acc cag gag cag aac aag gag aat ctg aac   624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

ccc aat tct gac gcg cct gtc atc cgg tca aaa acc tcc gcg cgc tac   672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag   720
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct   768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag   816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct   864
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg   912
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc   960
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc  1008
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc  1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat  1104
```

```
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc   1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc   1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg   1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc   1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt   1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag   1392
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg   1440
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc   1488
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc   1536
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc   1584
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

gac agg tac caa aac aaa tgt tct cgt cac gcg ggc atg ctt cag atg   1632
Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540

ctg ttt ccc tgc aag aca tgc gag aga atg aat cag aat ttc aac att   1680
```

```
Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg   1728
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt   1776
Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590

gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc   1824
Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595                 600                 605

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa   1872
Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 5
<211> 623
<212> PRT
<213> AAV-1

<400> 5

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1               5                  10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
```

115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
165 170 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
275 280 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala

370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 6
<211> 1641
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1638)

<400> 6

```
atg ccg ggc ttc tac gag atc gtg atc aag gtg ccg agc gac ctg gac    48
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
  1               5                  10                  15

gag cac ctg ccg ggc att tct gac tcg ttt gtg agc tgg gtg gcc gag    96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ctg ccc ccg gat tct gac atg gat ctg aat ctg att   144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttc ctg   192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

gtc caa tgg cgc cgc gtg agt aag gcc ccg gag gcc ctc ttc ttt gtt   240
Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

cag ttc gag aag ggc gag tcc tac ttc cac ctc cat att ctg gtg gag   288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

acc acg ggg gtc aaa tcc atg gtg ctg ggc cgc ttc ctg agt cag att   336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

agg gac aag ctg gtg cag acc atc tac cgc ggg atc gag ccg acc ctg   384
Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

ccc aac tgg ttc gcg gtg acc aag acg cgt aat ggc gcc gga ggg ggg   432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

aac aag gtg gtg gac gag tgc tac atc ccc aac tac ctc ctg ccc aag   480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
```

```
145                 150                 155                 160

act cag ccc gag ctg cag tgg gcg tgg act aac atg gag gag tat ata   528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

agc gcc tgt ttg aac ctg gcc gag cgc aaa cgg ctc gtg gcg cag cac   576
Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acc cac gtc agc cag acc cag gag cag aac aag gag aat ctg aac   624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

ccc aat tct gac gcg cct gtc atc cgg tca aaa acc tcc gcg cgc tac   672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag   720
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct   768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag   816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct   864
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg   912
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc   960
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc   1008
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc   1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
```

```
                340                 345                 350

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat   1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc   1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc   1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg   1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc   1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt   1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag   1392
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg   1440
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc   1488
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc   1536
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc   1584
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa   1632
Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
```

530 535 540

cct ctc tga 1641
Pro Leu
545

<210> 7
<211> 546
<212> PRT
<213> AAV-1

<400> 7

Met	Pro	Gly	Phe	Tyr	Glu	Ile	Val	Ile	Lys	Val	Pro	Ser	Asp	Leu	Asp
1				5				10					15		
Glu	His	Leu	Pro	Gly	Ile	Ser	Asp	Ser	Phe	Val	Ser	Trp	Val	Ala	Glu
			20					25					30		
Lys	Glu	Trp	Glu	Leu	Pro	Pro	Asp	Ser	Asp	Met	Asp	Leu	Asn	Leu	Ile
		35					40					45			
Glu	Gln	Ala	Pro	Leu	Thr	Val	Ala	Glu	Lys	Leu	Gln	Arg	Asp	Phe	Leu
	50					55					60				
Val	Gln	Trp	Arg	Arg	Val	Ser	Lys	Ala	Pro	Glu	Ala	Leu	Phe	Phe	Val
65					70					75					80
Gln	Phe	Glu	Lys	Gly	Glu	Ser	Tyr	Phe	His	Leu	His	Ile	Leu	Val	Glu
				85					90					95	
Thr	Thr	Gly	Val	Lys	Ser	Met	Val	Leu	Gly	Arg	Phe	Leu	Ser	Gln	Ile
			100					105					110		
Arg	Asp	Lys	Leu	Val	Gln	Thr	Ile	Tyr	Arg	Gly	Ile	Glu	Pro	Thr	Leu
		115					120					125			
Pro	Asn	Trp	Phe	Ala	Val	Thr	Lys	Thr	Arg	Asn	Gly	Ala	Gly	Gly	Gly
	130					135					140				
Asn	Lys	Val	Val	Asp	Glu	Cys	Tyr	Ile	Pro	Asn	Tyr	Leu	Leu	Pro	Lys
145					150					155					160
Thr	Gln	Pro	Glu	Leu	Gln	Trp	Ala	Trp	Thr	Asn	Met	Glu	Glu	Tyr	Ile
				165					170					175	
Ser	Ala	Cys	Leu	Asn	Leu	Ala	Glu	Arg	Lys	Arg	Leu	Val	Ala	Gln	His
			180					185					190		

```
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445
```

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
530 535 540

Pro Leu
545

<210> 8
<211> 1200
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1197)

<400> 8
atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag 48
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1 5 10 15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct 96
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag 144
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct 192
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
50 55 60

```
ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg   240
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
 65                  70                  75                  80

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc   288
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc   336
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc   384
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat   432
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc   480
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc   528
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg   576
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc   624
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt   672
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag   720
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg   768
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
                245                 250                 255
```

```
gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc   816
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
            260                 265                 270

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc   864
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc   912
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

gac agg tac caa aac aaa tgt tct cgt cac gcg ggc atg ctt cag atg   960
Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
305                 310                 315                 320

ctg ttt ccc tgc aag aca tgc gag aga atg aat cag aat ttc aac att   1008
Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
                325                 330                 335

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg   1056
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
            340                 345                 350

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt   1104
Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
        355                 360                 365

gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc   1152
Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
    370                 375                 380

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa   1200
Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
385                 390                 395
```

<210> 9
<211> 399
<212> PRT
<213> AAV-1

<400> 9

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
  1               5                  10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
```

20 25 30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
50 55 60

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65 70 75 80

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
85 90 95

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
245 250 255

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
260 265 270

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val

```
          275                 280                 285

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
305                 310                 315                 320

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
                325                 330                 335

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
            340                 345                 350

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
        355                 360                 365

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
    370                 375                 380

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
385                 390                 395
```

<210> 10
<211> 969
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(966)

<220>
<221> misc_feature
<222> (943)..(944)
<223> minor splice site

<400> 10

```
atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag   48
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
  1               5                  10                  15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct   96
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag   144
```

```
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
          35                  40                  45

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct   192
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
     50                  55                  60

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg   240
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
 65                  70                  75                  80

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc   288
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                 85                  90                  95

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc   336
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc   384
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat   432
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc   480
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc   528
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg   576
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc   624
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt   672
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag   720
```

```
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg   768
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
                245                 250                 255

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc   816
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
            260                 265                 270

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc   864
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc   912
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa   960
Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
305                 310                 315                 320

cct ctc tga                                                      969
Pro Leu
```

<210> 11
<211> 322
<212> PRT
<213> AAV-1

<400> 11

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
  1               5                  10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35                  40                  45

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
    50                  55                  60

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65                  70                  75                  80
```

```
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
                245                 250                 255

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
            260                 265                 270

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
305                 310                 315                 320

Pro Leu
```

<210> 12
<211> 2211
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(2208)

<400> 12

```
atg gct gcc gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct    48
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
  1               5                  10                  15

gag ggc att cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc    96
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
             20                  25                  30

aaa gcc aac cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct   144
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
         35                  40                  45

ggc tac aag tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc   192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
     50                  55                  60

gtc aac gcg gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac   240
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
 65                  70                  75                  80

cag cag ctc aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc   288
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                 85                  90                  95

gac gcc gag ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc   336
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

aac ctc ggg cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct   384
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

ctc ggt ctg gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt   432
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

ccg gta gag cag tcg cca caa gag cca gac tcc tcc tcg ggc atc ggc   480
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

aag aca ggc cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act   528
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

ggc gac tca gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca   576
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

gca acc ccc gct gct gtg gga cct act aca atg gct tca ggc ggt ggc   624
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

gca cca atg gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc   672
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

tca gga aat tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc   720
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

acc acc agc acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc   768
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

tac aag caa atc tcc agt gct tca acg ggg gcc agc aac gac aac cac   816
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

tac ttc ggc tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc   864
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

cac tgc cac ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat   912
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

tgg gga ttc cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa   960
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

gtc aag gag gtc acg acg aat gat ggc gtc aca acc atc gct aat aac  1008
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

ctt acc agc acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg  1056
```

```
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

tac gtc ctc ggc tct gcg cac cag ggc tgc ctc cct ccg ttc ccg gcg   1104
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

gac gtg ttc atg att ccg caa tac ggc tac ctg acg ctc aac aat ggc   1152
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

agc caa gcc gtg gga cgt tca tcc ttt tac tgc ctg gaa tat ttc cct   1200
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

tct cag atg ctg aga acg ggc aac aac ttt acc ttc agc tac acc ttt   1248
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

gag gaa gtg cct ttc cac agc agc tac gcg cac agc cag agc ctg gac   1296
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

cgg ctg atg aat cct ctc atc gac caa tac ctg tat tac ctg aac aga   1344
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

act caa aat cag tcc gga agt gcc caa aac aag gac ttg ctg ttt agc   1392
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

cgt ggg tct cca gct ggc atg tct gtt cag ccc aaa aac tgg cta cct   1440
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

gga ccc tgt tat cgg cag cag cgc gtt tct aaa aca aaa aca gac aac   1488
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

aac aac agc aat ttt acc tgg act ggt gct tca aaa tat aac ctc aat   1536
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

ggg cgt gaa tcc atc atc aac cct ggc act gct atg gcc tca cac aaa   1584
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

gac gac gaa gac aag ttc ttt ccc atg agc ggt gtc atg att ttt gga   1632
```

```
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

aaa gag agc gcc gga gct tca aac act gca ttg gac aat gtc atg att   1680
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

aca gac gaa gag gaa att aaa gcc act aac cct gtg gcc acc gaa aga   1728
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

ttt ggg acc gtg gca gtc aat ttc cag agc agc agc aca gac cct gcg   1776
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

acc gga gat gtg cat gct atg gga gca tta cct ggc atg gtg tgg caa   1824
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

gat aga gac gtg tac ctg cag ggt ccc att tgg gcc aaa att cct cac   1872
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

aca gat gga cac ttt cac ccg tct cct ctt atg ggc ggc ttt gga ctc   1920
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

aag aac ccg cct cct cag atc ctc atc aaa aac acg cct gtt cct gcg   1968
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

aat cct ccg gcg gag ttt tca gct aca aag ttt gct tca ttc atc acc   2016
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

caa tac tcc aca gga caa gtg agt gtg gaa att gaa tgg gag ctg cag   2064
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

aaa gaa aac agc aag cgc tgg aat ccc gaa gtg cag tac aca tcc aat   2112
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

tat gca aaa tct gcc aac gtt gat ttt act gtg gac aac aat gga ctt   2160
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

tat act gag cct cgc ccc att ggc acc cgt tac ctt acc cgt ccc ctg   2208
```

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

taa 2211

<210> 13
<211> 736
<212> PRT
<213> AAV-1

<400> 13
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

```
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445
```

```
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700
```

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 14
<211> 1800
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1797)

<400> 14

```
acg gct cct gga aag aaa cgt ccg gta gag cag tcg cca caa gag cca   48
Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro
  1               5                  10                  15

gac tcc tcc tcg ggc atc ggc aag aca ggc cag cag ccc gct aaa aag   96
Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys
             20                  25                  30

aga ctc aat ttt ggt cag act ggc gac tca gag tca gtc ccc gat cca   144
Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro
         35                  40                  45

caa cct ctc gga gaa cct cca gca acc ccc gct gct gtg gga cct act   192
Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr
     50                  55                  60

aca atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc   240
Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
 65                  70                  75                  80

gcc gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca   288
Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr
                 85                  90                  95

tgg ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg   336
Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
            100                 105                 110

ccc acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg   384
Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr
        115                 120                 125
```

```
ggg gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg   432
Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
    130                 135                 140

tat ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg   480
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
145                 150                 155                 160

cag cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac   528
Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
                165                 170                 175

ttc aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc   576
Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly
            180                 185                 190

gtc aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg   624
Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser
        195                 200                 205

gac tcg gag tac cag ctt ccg tac gtc ctc ggc tct gcg cac cag ggc   672
Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
    210                 215                 220

tgc ctc cct ccg ttc ccg gcg gac gtg ttc atg att ccg caa tac ggc   720
Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
225                 230                 235                 240

tac ctg acg ctc aac aat ggc agc caa gcc gtg gga cgt tca tcc ttt   768
Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
                245                 250                 255

tac tgc ctg gaa tat ttc cct tct cag atg ctg aga acg ggc aac aac   816
Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
            260                 265                 270

ttt acc ttc agc tac acc ttt gag gaa gtg cct ttc cac agc agc tac   864
Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr
        275                 280                 285

gcg cac agc cag agc ctg gac cgg ctg atg aat cct ctc atc gac caa   912
Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
    290                 295                 300

tac ctg tat tac ctg aac aga act caa aat cag tcc gga agt gcc caa   960
Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln
305                 310                 315                 320
```

```
aac aag gac ttg ctg ttt agc cgt ggg tct cca gct ggc atg tct gtt   1008
Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val
                325                 330                 335

cag ccc aaa aac tgg cta cct gga ccc tgt tat cgg cag cag cgc gtt   1056
Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val
            340                 345                 350

tct aaa aca aaa aca gac aac aac aac agc aat ttt acc tgg act ggt   1104
Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly
        355                 360                 365

gct tca aaa tat aac ctc aat ggg cgt gaa tcc atc atc aac cct ggc   1152
Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly
    370                 375                 380

act gct atg gcc tca cac aaa gac gac gaa gac aag ttc ttt ccc atg   1200
Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met
385                 390                 395                 400

agc ggt gtc atg att ttt gga aaa gag agc gcc gga gct tca aac act   1248
Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr
                405                 410                 415

gca ttg gac aat gtc atg att aca gac gaa gag gaa att aaa gcc act   1296
Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr
            420                 425                 430

aac cct gtg gcc acc gaa aga ttt ggg acc gtg gca gtc aat ttc cag   1344
Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln
        435                 440                 445

agc agc agc aca gac cct gcg acc gga gat gtg cat gct atg gga gca   1392
Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala
    450                 455                 460

tta cct ggc atg gtg tgg caa gat aga gac gtg tac ctg cag ggt ccc   1440
Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
465                 470                 475                 480

att tgg gcc aaa att cct cac aca gat gga cac ttt cac ccg tct cct   1488
Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro
                485                 490                 495

ctt atg ggc ggc ttt gga ctc aag aac ccg cct cct cag atc ctc atc   1536
Leu Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile
            500                 505                 510
```

```
aaa aac acg cct gtt cct gcg aat cct ccg gcg gag ttt tca gct aca   1584
Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr
        515                 520                 525

aag ttt gct tca ttc atc acc caa tac tcc aca gga caa gtg agt gtg   1632
Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
    530                 535                 540

gaa att gaa tgg gag ctg cag aaa gaa aac agc aag cgc tgg aat ccc   1680
Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
545                 550                 555                 560

gaa gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt   1728
Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe
                565                 570                 575

act gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc   1776
Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr
            580                 585                 590

cgt tac ctt acc cgt ccc ctg taa                                  1800
Arg Tyr Leu Thr Arg Pro Leu
        595
```

<210> 15
<211> 599
<212> PRT
<213> AAV-1

<400> 15

```
Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro
  1               5                  10                  15

Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys
             20                  25                  30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro
         35                  40                  45

Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr
     50                  55                  60

Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
 65                  70                  75                  80

Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr
```

85 90 95

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
100 105 110

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr
115 120 125

Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
130 135 140

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
145 150 155 160

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
165 170 175

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly
180 185 190

Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser
195 200 205

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
210 215 220

Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
225 230 235 240

Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
245 250 255

Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
260 265 270

Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr
275 280 285

Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
290 295 300

Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln
305 310 315 320

Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val
325 330 335

Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val

340 345 350

Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly
355 360 365

Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly
370 375 380

Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met
385 390 395 400

Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr
405 410 415

Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr
420 425 430

Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln
435 440 445

Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala
450 455 460

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
465 470 475 480

Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro
485 490 495

Leu Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile
500 505 510

Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr
515 520 525

Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
530 535 540

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
545 550 555 560

Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe
565 570 575

Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr
580 585 590

Arg Tyr Leu Thr Arg Pro Leu

595

<210> 16
<211> 1605
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1602)

<400> 16

```
atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc gcc   48
Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
 1               5                  10                  15

gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca tgg   96
Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp
            20                  25                  30

ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg ccc   144
Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
        35                  40                  45

acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg ggg   192
Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly
    50                  55                  60

gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg tat   240
Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65                  70                  75                  80

ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg cag   288
Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
                85                  90                  95

cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac ttc   336
Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe
            100                 105                 110

aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc gtc   384
Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val
        115                 120                 125

aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg gac   432
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp
    130                 135                 140
```

```
tcg gag tac cag ctt ccg tac gtc ctc ggc tct gcg cac cag ggc tgc    480
Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys
145                 150                 155                 160

ctc cct ccg ttc ccg gcg gac gtg ttc atg att ccg caa tac ggc tac    528
Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr
                165                 170                 175

ctg acg ctc aac aat ggc agc caa gcc gtg gga cgt tca tcc ttt tac    576
Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr
            180                 185                 190

tgc ctg gaa tat ttc cct tct cag atg ctg aga acg ggc aac aac ttt    624
Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
        195                 200                 205

acc ttc agc tac acc ttt gag gaa gtg cct ttc cac agc agc tac gcg    672
Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala
    210                 215                 220

cac agc cag agc ctg gac cgg ctg atg aat cct ctc atc gac caa tac    720
His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
225                 230                 235                 240

ctg tat tac ctg aac aga act caa aat cag tcc gga agt gcc caa aac    768
Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn
                245                 250                 255

aag gac ttg ctg ttt agc cgt ggg tct cca gct ggc atg tct gtt cag    816
Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln
            260                 265                 270

ccc aaa aac tgg cta cct gga ccc tgt tat cgg cag cag cgc gtt tct    864
Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
        275                 280                 285

aaa aca aaa aca gac aac aac aac agc aat ttt acc tgg act ggt gct    912
Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala
    290                 295                 300

tca aaa tat aac ctc aat ggg cgt gaa tcc atc atc aac cct ggc act    960
Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr
305                 310                 315                 320

gct atg gcc tca cac aaa gac gac gaa gac aag ttc ttt ccc atg agc   1008
Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser
                325                 330                 335
```

```
ggt gtc atg att ttt gga aaa gag agc gcc gga gct tca aac act gca   1056
Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala
            340                 345                 350

ttg gac aat gtc atg att aca gac gaa gag gaa att aaa gcc act aac   1104
Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
        355                 360                 365

cct gtg gcc acc gaa aga ttt ggg acc gtg gca gtc aat ttc cag agc   1152
Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser
    370                 375                 380

agc agc aca gac cct gcg acc gga gat gtg cat gct atg gga gca tta   1200
Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu
385                 390                 395                 400

cct ggc atg gtg tgg caa gat aga gac gtg tac ctg cag ggt ccc att   1248
Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
                405                 410                 415

tgg gcc aaa att cct cac aca gat gga cac ttt cac ccg tct cct ctt   1296
Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
            420                 425                 430

atg ggc ggc ttt gga ctc aag aac ccg cct cct cag atc ctc atc aaa   1344
Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys
        435                 440                 445

aac acg cct gtt cct gcg aat cct ccg gcg gag ttt tca gct aca aag   1392
Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys
    450                 455                 460

ttt gct tca ttc atc acc caa tac tcc aca gga caa gtg agt gtg gaa   1440
Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
465                 470                 475                 480

att gaa tgg gag ctg cag aaa gaa aac agc aag cgc tgg aat ccc gaa   1488
Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
                485                 490                 495

gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt act   1536
Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr
            500                 505                 510

gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc cgt   1584
Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
        515                 520                 525
```

tac ctt acc cgt ccc ctg taa 1605
Tyr Leu Thr Arg Pro Leu
530

<210> 17
<211> 534
<212> PRT
<213> AAV-1

<400> 17

Met	Ala	Ser	Gly	Gly	Gly	Ala	Pro	Met	Ala	Asp	Asn	Asn	Glu	Gly	Ala
1				5				10				15			
Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Thr	Trp
			20					25				30			
Leu	Gly	Asp	Arg	Val	Ile	Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro
		35					40					45			
Thr	Tyr	Asn	Asn	His	Leu	Tyr	Lys	Gln	Ile	Ser	Ser	Ala	Ser	Thr	Gly
	50					55					60				
Ala	Ser	Asn	Asp	Asn	His	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr
65					70					75					80
Phe	Asp	Phe	Asn	Arg	Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln
				85					90					95	
Arg	Leu	Ile	Asn	Asn	Asn	Trp	Gly	Phe	Arg	Pro	Lys	Arg	Leu	Asn	Phe
			100					105					110		
Lys	Leu	Phe	Asn	Ile	Gln	Val	Lys	Glu	Val	Thr	Thr	Asn	Asp	Gly	Val
		115					120					125			
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Ser	Asp
	130					135					140				
Ser	Glu	Tyr	Gln	Leu	Pro	Tyr	Val	Leu	Gly	Ser	Ala	His	Gln	Gly	Cys
145					150					155					160
Leu	Pro	Pro	Phe	Pro	Ala	Asp	Val	Phe	Met	Ile	Pro	Gln	Tyr	Gly	Tyr
				165					170					175	
Leu	Thr	Leu	Asn	Asn	Gly	Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr
			180					185					190		

```
Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
        195                 200                 205

Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala
    210                 215                 220

His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
225                 230                 235                 240

Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn
                245                 250                 255

Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln
            260                 265                 270

Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
        275                 280                 285

Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala
    290                 295                 300

Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr
305                 310                 315                 320

Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser
                325                 330                 335

Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala
            340                 345                 350

Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
        355                 360                 365

Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser
    370                 375                 380

Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu
385                 390                 395                 400

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
                405                 410                 415

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
            420                 425                 430

Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys
        435                 440                 445
```

Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys
450 455 460

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
465 470 475 480

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
485 490 495

Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr
500 505 510

Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
515 520 525

Tyr Leu Thr Arg Pro Leu
530

<210> 18
<211> 4681
<212> DNA
<213> aav-2

<400> 18
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg 360

accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg 420

aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga 480

ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 540

cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc 600

tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg 660

aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg 720

tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc 780

ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac 840

agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga 900

cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc 960

cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020

aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080

atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta 1140

tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt 1200

ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt 1260

ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320

ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380

acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440

tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500

tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga 1560

ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620

ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc 1680

tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agacttttc cggtgggcaa 1740

aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa 1800

gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc 1860

agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat 1920

gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga 1980

atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg 2040

tgtcagaatc tcaaccggtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc 2100

atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt 2160

tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat 2220

cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa 2280

cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg 2340

cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac 2400

gaggcagacg ccgcggccct cgagcacgac aaagcctacg accggcagct cgacagcgga 2460

gacaacccgt acctcaagta caaccacgcc gacgcggagt ttcaggagcg ccttaaagaa 2520

gatacgtctt ttgggggcaa cctcggacga gcagtcttcc aggcgaaaaa gagggttctt 2580

gaacctctcg gcctggttga ggaacctgtt aagacggctc cgggaaaaaa gaggccggta 2640

gagcactctc ctgtggagcc agactcctcc tcgggaaccg gaaagccggg ccagcagcct 2700

gcaagaaaaa gattgaattt tggtcagact ggagacgcag actcagtacc tgacccccag 2760

cctctcggac agccaccagc agccccctct ggtctgggaa ctaatacgat ggctacaggc 2820

agtggcgcac caatggcaga caataacgag ggcgccgacg gagtgggtaa ttcctccgga 2880

aattggcatt gcgattccac atggatgggc gacagagtca tcaccaccag cacccgaacc 2940

tgggccctgc ccacctacaa caaccacctc tacaaacaaa tttccagcca atcaggagcc 3000

tcgaacgaca atcactactt tggctacagc acccccttggg ggtattttga cttcaacaga 3060

ttccactgcc acttttcacc acgtgactgg caaagactca tcaacaacaa ctggggattc 3120

cgacccaaga gactcaactt caacctcttt aacattcaag tcaaagaggt cacgcagaat 3180

gacggtacga cgacgattgc caataacctt accagcacgg ttcaggtgtt tactgactcg 3240

gagtaccagc tcccgtacgt cctcggctcg gcgcatcaag gatgcctccc gccgttccca 3300

gcagacgtct tcatggtgcc acagtatgga tacctcaccc tgaacaacgg gagtcaggca 3360

gtaggacgct cttcatttta ctgcctggag tactttcctt ctcagatgct gcgtaccgga 3420

aacaacttta ccttcagcta cacttttgag gacgttcctt tccacagcag ctacgctcac 3480

agccagagtc tggaccgtct catgaatcct ctcatcgacc agtacctgta ttacttgagc 3540

agaacaaaca ctccaagtgg aaccaccacg cagtcaaggc ttcagttttc tcaggcccca 3600

gccagtgaca ttcgggacca gtctaggaac tggcttcctg gaccctgtta ccgccagcag 3660

cgagtatgaa agacatctgc ggataacaac aacagtgaat actcgtggac tggagctacc 3720

aagtaccacc tcaatggcag agactctctg gtgaatccgg ggcccgccat ggcaagccac 3780

aaggacgatg aagaaaagtt ttttcctcag agcggggttc tcatctttgg gaagcaaggc 3840

tcagagaaaa caaatgtgaa cattgaaaag gtcatgatta cagacgaaga ggaaatccca 3900

acaaccaatc ccgtggctac ggagcagtat ggttctgtat ctaccaacct ccagagaggc 3960

aacagacaag cagctaccgc agatgtcaac acacaaggcg ttcttccagg catggtctgg 4020

caggacagag atgtgtacct tcaggggccc atctgggcaa agattccaca cacggacgga 4080

cattttcacc cctctccccc catgggtgga ttcggactta aacaccctcc tccacagatt 4140

ctcatcaaga acaccccggt acctgcgaat ccttcgacca ccttcagtgc ggcaaagttt 4200

gcttccttca tcacacagta ctccacggga cacggtcagc gtggagatcg agtgggagct 4260

gcagaacgaa aacagcaaac gctggaatcc cgaaattcag tacacttcca actacaacaa 4320

gtctgttaat cgtggacttt accgtggata ctaatggcgt gtattcagag cctcgcccca 4380

ttggcaccag atacctgact cgtaatctgt aattgcttgt taatcaataa accgtttaat 4440

tcgtttcagt tgaactttgg tctctgcgta tttctttctt atctagtttc catggctacg 4500

tagataagta gcatggcggg ttaatcatta actacaagga acccctagtg atggagttgg 4560

ccactccctc tctgcgcgct cgctcgctca ctgaggccgg gcgaccaaag gtcgcccgac 4620

gcccgggctt tgccccggcg gcctcagtga gcgagcgagc gcgcagagag ggagtgggca 4680

a 4681

<210> 19
<211> 4683
<212> DNA
<213> aav-6

<400> 19
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagcgcca tgccggggtt ttacgagatt gtgattaagg tccccagcga 360

ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga 420

atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg caccctgac 480

cgtggccgag aagctgcagc gcgacttcct ggtccactgg cgccgcgtga gtaaggcccc 540

ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct 600

ggtggagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc agattagcga 660

caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt 720

gaccaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt gctacatccc 780

caactacctc ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta acatggagga 840

gtatataagc gcgtgtttaa acctggccga gcgcaaacgg ctcgtggcgc acgacctgac 900

ccacgtcagc cagacccagg agcagaacaa ggagaatctg aaccccaatt ctgacgcgcc 960

tgtcatccgg tcaaaaacct ccgcacgcta catggagctg gtcgggtggc tggtggaccg 1020

gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca tctccttcaa 1080

cgccgcctcc aactcgcggt cccagatcaa ggccgctctg gacaatgccg gcaagatcat 1140

ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctccgcccg ccgacattaa 1200

aaccaaccgc atttaccgca tcctggagct gaacggctac gaccctgcct acgccggctc 1260

cgtctttctc ggctgggccc agaaaaggtt cggaaaacgc aacaccatct ggctgtttgg 1320

gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg tgcccttcta 1380

cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg acaagatggt 1440

gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca aggccattct 1500

cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatcccac 1560

ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 1620

cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactca cccgccgtct 1680

ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 1740

ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag ccaacaacag 1800

acccgccccc gatgacgcgg ataaaagcga gcccaagcgg gcctgccccc cagtcgcgga 1860

tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1920

atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat gcgagagaat 1980

gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag aatgtttccc 2040

cggcgtgtca gaatctcaac cggtcgtcag aaagaggacg tatcggaaac tctgtgccat 2100

tcatcatctg ctggggcggg ctcccgagat tgcttgctcg gcctgcgatc tggtcaacgt 2160

ggatctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg gctgccgatg 2220

gttatcttcc agattggctc gaggacaacc tctctgaggg cattcggcag tggtgggact 2280

tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 2340

tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag ggggagcccg 2400

tcaacgcggc ggatgcagcg gccctcgagc acgacaaggc ctacgaccag cagctcaaag 2460

cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag gagcgtctgc 2520

aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagaggg 2580

ttctcgaacc ttttggtctg gttgaggaag gtgctaagac ggctcctgga aagaaacgtc 2640

cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag acaggccagc 2700

agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca gtccccgacc 2760

cacaacctct cggagaacct ccagcaaccc ccgctgctgt gggacctact acaatggctt 2820

caggcggtgg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg ggtaatgcct 2880

caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc accagcaccc 2940

gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaatctcc agtgcttcaa 3000

cgggggccag caacgacaac cactacttcg gctacagcac cccctggggg tattttgatt 3060

tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc aacaacaatt 3120

ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc aaggaggtca 3180

cgacgaatga tggcgtcacg accatcgcta ataaccttac cagcacggtt caagtcttgt 3240

cggactcgga gtaccagttc ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 3300

cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc aacaatggca 3360

gccaggcagt gggacgctca tccttttact gcctggaata tttcccatcg cagatgctga 3420

gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc cacagcagct 3480

acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag tacctgtatt 3540

acctgaacag aactcacaat cagtccggaa gtgcccaaaa caaggacttg ctgtttagcc 3600

gtgggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga ccctgttacc 3660

ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaacttt acctggactg 3720

gtgcttcaaa atataacctt aatgggcgtg aatctataat caaccctggc actgctatgg 3780

cctcacacaa agacgacaaa gacaagttct ttcccatgag cggtgtcatg atttttggaa 3840

aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca gacgaagagg 3900

aaatcaaagc cactaacccc gtggccaccg aaagatttgg gactgtggca gtcaatctcc 3960

agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc ttacctggaa 4020

tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa attcctcaca 4080

cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag cacccgcctc 4140

ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag ttttcggcta 4200

caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg gagattgaat 4260

gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat acatctaact 4320

atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat actgagcctc 4380

gccccattgg cacccgttac ctcacccgtc ccctgtaatt gtgtgttaat caataaaccg 4440

gttaattcgt gtcagttgaa ctttggtctc atgtccttat tatcttatct ggtcaccata 4500

gcaaccggtt acacattaac tgcttagttg cgcttcgcga ataccctag tgatggagtt 4560

gcccactccc tctatgcgcg ctcgctcgct cggtggggcc ggcagagcag agctctgccg 4620

tctgcggacc tttggtccgc aggccccacc gagcgagcga gcgcgcatag agggagtggc 4680

caa 4683

<210> 20
<211> 16
<212> DNA
<213> rep binding motif

<400> 20
gctcgctcgc tcgctg 16

SEQUENCE LISTING

<110> Wilson, James M.
Xiao, Weidong

<120> Adeno-Associated Virus Serotype I Nucleic Acid Sequences, Vectors and Host Cells Containing Same

<130> GNVPN.031USA

<140> US 09/807,802
<141> 2001-04-17

<150> US 60/107,114
<151> 1998-11-05

<150> PCT/US99/25694
<151> 1999-11-02

<160> 20

<170> PatentIn version 3.1

<210> 1
<211> 4718
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (335)..(2206)
<223>

<220>
<221> CDS
<222> (2223)..(4430)
<223>

<400> 1
ttgcccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60

agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcag agagggagtg 120

ggcaactcca tcactagggg taatcgcgaa gcgcctccca cgctgccgcg tcagcgctga 180

cgtaaattac gtcatagggg agtggtcctg tattagctgt cacgtgagtg cttttgcgac 240

attttgcgac accacgtggc catttagggt atatatggcc gagtgagcga gcaggatctc 300

cattttgacc gcgaaatttg aacgagcagc agcc atg ccg ggc ttc tac gag atc 355
Met Pro Gly Phe Tyr Glu Ile
1 5

gtg atc aag gtg ccg agc gac ctg gac gag cac ctg ccg ggc att tct 403
Val Ile Lys Val Pro Ser Asp Leu Asp Glu His Leu Pro Gly Ile Ser
10 15 20

gac tcg ttt gtg agc tgg gtg gcc gag aag gaa tgg gag ctg ccc ccg 451
Asp Ser Phe Val Ser Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro
25 30 35

```
gat tct gac atg gat ctg aat ctg att gag cag gca ccc ctg acc gtg      499
Asp Ser Asp Met Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val
40                  45                  50                  55

gcc gag aag ctg cag cgc gac ttc ctg gtc caa tgg cgc cgc gtg agt      547
Ala Glu Lys Leu Gln Arg Asp Phe Leu Val Gln Trp Arg Arg Val Ser
                60                  65                  70

aag gcc ccg gag gcc ctc ttc ttt gtt cag ttc gag aag ggc gag tcc      595
Lys Ala Pro Glu Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser
            75                  80                  85

tac ttc cac ctc cat att ctg gtg gag acc acg ggg gtc aaa tcc atg      643
Tyr Phe His Leu His Ile Leu Val Glu Thr Thr Gly Val Lys Ser Met
        90                  95                  100

gtg ctg ggc cgc ttc ctg agt cag att agg gac aag ctg gtg cag acc      691
Val Leu Gly Arg Phe Leu Ser Gln Ile Arg Asp Lys Leu Val Gln Thr
    105                 110                 115

atc tac cgc ggg atc gag ccg acc ctg ccc aac tgg ttc gcg gtg acc      739
Ile Tyr Arg Gly Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr
120                 125                 130                 135

aag acg cgt aat ggc gcc gga ggg ggg aac aag gtg gtg gac gag tgc      787
Lys Thr Arg Asn Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys
                140                 145                 150

tac atc ccc aac tac ctc ctg ccc aag act cag ccc gag ctg cag tgg      835
Tyr Ile Pro Asn Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp
            155                 160                 165

gcg tgg act aac atg gag gag tat ata agc gcc tgt ttg aac ctg gcc      883
Ala Trp Thr Asn Met Glu Glu Tyr Ile Ser Ala Cys Leu Asn Leu Ala
        170                 175                 180

gag cgc aaa cgg ctc gtg gcg cag cac ctg acc cac gtc agc cag acc      931
Glu Arg Lys Arg Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr
    185                 190                 195

cag gag cag aac aag gag aat ctg aac ccc aat tct gac gcg cct gtc      979
Gln Glu Gln Asn Lys Glu Asn Leu Asn Pro Asn Ser Asp Ala Pro Val
200                 205                 210                 215

atc cgg tca aaa acc tcc gcg cgc tac atg gag ctg gtc ggg tgg ctg     1027
Ile Arg Ser Lys Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu
                220                 225                 230

gtg gac cgg ggc atc acc tcc gag aag cag tgg atc cag gag gac cag     1075
Val Asp Arg Gly Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln
            235                 240                 245

gcc tcg tac atc tcc ttc aac gcc gct tcc aac tcg cgg tcc cag atc     1123
Ala Ser Tyr Ile Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile
        250                 255                 260

aag gcc gct ctg gac aat gcc ggc aag atc atg gcg ctg acc aaa tcc     1171
Lys Ala Ala Leu Asp Asn Ala Gly Lys Ile Met Ala Leu Thr Lys Ser
    265                 270                 275
```

```
gcg ccc gac tac ctg gta ggc ccc gct ccg ccc gcg gac att aaa acc      1219
Ala Pro Asp Tyr Leu Val Gly Pro Ala Pro Pro Ala Asp Ile Lys Thr
280                 285                 290                 295

aac cgc atc tac cgc atc ctg gag ctg aac ggc tac gaa cct gcc tac      1267
Asn Arg Ile Tyr Arg Ile Leu Glu Leu Asn Gly Tyr Glu Pro Ala Tyr
                300                 305                 310

gcc ggc tcc gtc ttt ctc ggc tgg gcc cag aaa agg ttc ggg aag cgc      1315
Ala Gly Ser Val Phe Leu Gly Trp Ala Gln Lys Arg Phe Gly Lys Arg
            315                 320                 325

aac acc atc tgg ctg ttt ggg ccg gcc acc acg ggc aag acc aac atc      1363
Asn Thr Ile Trp Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile
        330                 335                 340

gcg gaa gcc atc gcc cac gcc gtg ccc ttc tac ggc tgc gtc aac tgg      1411
Ala Glu Ala Ile Ala His Ala Val Pro Phe Tyr Gly Cys Val Asn Trp
    345                 350                 355

acc aat gag aac ttt ccc ttc aat gat tgc gtc gac aag atg gtg atc      1459
Thr Asn Glu Asn Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile
360                 365                 370                 375

tgg tgg gag gag ggc aag atg acg gcc aag gtc gtg gag tcc gcc aag      1507
Trp Trp Glu Glu Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys
                380                 385                 390

gcc att ctc ggc ggc agc aag gtg cgc gtg gac caa aag tgc aag tcg      1555
Ala Ile Leu Gly Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser
            395                 400                 405

tcc gcc cag atc gac ccc acc ccc gtg atc gtc acc tcc aac acc aac      1603
Ser Ala Gln Ile Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn
        410                 415                 420

atg tgc gcc gtg att gac ggg aac agc acc acc ttc gag cac cag cag      1651
Met Cys Ala Val Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln
    425                 430                 435

ccg ttg cag gac cgg atg ttc aaa ttt gaa ctc acc cgc cgt ctg gag      1699
Pro Leu Gln Asp Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Glu
440                 445                 450                 455

cat gac ttt ggc aag gtg aca aag cag gaa gtc aaa gag ttc ttc cgc      1747
His Asp Phe Gly Lys Val Thr Lys Gln Glu Val Lys Glu Phe Phe Arg
                460                 465                 470

tgg gcg cag gat cac gtg acc gag gtg gcg cat gag ttc tac gtc aga      1795
Trp Ala Gln Asp His Val Thr Glu Val Ala His Glu Phe Tyr Val Arg
            475                 480                 485

aag ggt gga gcc aac aaa aga ccc gcc ccc gat gac gcg gat aaa agc      1843
Lys Gly Gly Ala Asn Lys Arg Pro Ala Pro Asp Asp Ala Asp Lys Ser
        490                 495                 500

gag ccc aag cgg gcc tgc ccc tca gtc gcg gat cca tcg acg tca gac      1891
Glu Pro Lys Arg Ala Cys Pro Ser Val Ala Asp Pro Ser Thr Ser Asp
    505                 510                 515
```

```
gcg gaa gga gct ccg gtg gac ttt gcc gac agg tac caa aac aaa tgt      1939
Ala Glu Gly Ala Pro Val Asp Phe Ala Asp Arg Tyr Gln Asn Lys Cys
520                 525                 530                 535

tct cgt cac gcg ggc atg ctt cag atg ctg ttt ccc tgc aag aca tgc      1987
Ser Arg His Ala Gly Met Leu Gln Met Leu Phe Pro Cys Lys Thr Cys
                540                 545                 550

gag aga atg aat cag aat ttc aac att tgc ttc acg cac ggg acg aga      2035
Glu Arg Met Asn Gln Asn Phe Asn Ile Cys Phe Thr His Gly Thr Arg
            555                 560                 565

gac tgt tca gag tgc ttc ccc ggc gtg tca gaa tct caa ccg gtc gtc      2083
Asp Cys Ser Glu Cys Phe Pro Gly Val Ser Glu Ser Gln Pro Val Val
        570                 575                 580

aga aag agg acg tat cgg aaa ctc tgt gcc att cat cat ctg ctg ggg      2131
Arg Lys Arg Thr Tyr Arg Lys Leu Cys Ala Ile His His Leu Leu Gly
    585                 590                 595

cgg gct ccc gag att gct tgc tcg gcc tgc gat ctg gtc aac gtg gac      2179
Arg Ala Pro Glu Ile Ala Cys Ser Ala Cys Asp Leu Val Asn Val Asp
600                 605                 610                 615

ctg gat gac tgt gtt tct gag caa taa atgacttaaa ccaggt atg gct gcc    2231
Leu Asp Asp Cys Val Ser Glu Gln                     Met Ala Ala
                620                                 625

gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct gag ggc att      2279
Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu Gly Ile
            630                 635                 640

cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc aaa gcc aac      2327
Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro Lys Ala Asn
        645                 650                 655

cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct ggc tac aag      2375
Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro Gly Tyr Lys
    660                 665                 670

tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc gtc aac gcg      2423
Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro Val Asn Ala
675                 680                 685                 690

gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac cag cag ctc      2471
Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln Gln Leu
                695                 700                 705

aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc gac gcc gag      2519
Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala Asp Ala Glu
            710                 715                 720

ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc aac ctc ggg      2567
Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly Asn Leu Gly
        725                 730                 735

cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct ctc ggt ctg      2615
Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu Gly Leu
    740                 745                 750
```

```
gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt ccg gta gag      2663
Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg Pro Val Glu
755                 760                 765                 770

cag tcg cca caa gag cca gac tcc tcc tcg ggc atc ggc aag aca ggc      2711
Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly
                775                 780                 785

cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act ggc gac tca      2759
Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser
            790                 795                 800

gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca gca acc ccc      2807
Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro
        805                 810                 815

gct gct gtg gga cct act aca atg gct tca ggc ggt ggc gca cca atg      2855
Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly Ala Pro Met
    820                 825                 830

gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc tca gga aat      2903
Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asn
835                 840                 845                 850

tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc acc acc agc      2951
Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile Thr Thr Ser
                855                 860                 865

acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc tac aag caa      2999
Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln
            870                 875                 880

atc tcc agt gct tca acg ggg gcc agc aac gac aac cac tac ttc ggc      3047
Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His Tyr Phe Gly
        885                 890                 895

tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc cac tgc cac      3095
Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His
    900                 905                 910

ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat tgg gga ttc      3143
Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe
915                 920                 925                 930

cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa gtc aag gag      3191
Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu
                935                 940                 945

gtc acg acg aat gat ggc gtc aca acc atc gct aat aac ctt acc agc      3239
Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn Leu Thr Ser
            950                 955                 960

acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg tac gtc ctc      3287
Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu
        965                 970                 975

ggc tct gcg cac cag ggc tgc ctc cct ccg ttc ccg gcg gac gtg ttc      3335
Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe
    980                 985                 990
```

```
atg att ccg caa tac ggc  tac ctg acg ctc aac  aat ggc agc caa        3380
Met Ile Pro Gln Tyr Gly  Tyr Leu Thr Leu Asn  Asn Gly Ser Gln
995                 1000                1005

gcc  gtg gga cgt tca tcc  ttt tac tgc ctg gaa  tat ttc cct tct      3425
Ala  Val Gly Arg Ser Ser  Phe Tyr Cys Leu Glu  Tyr Phe Pro Ser
1010                1015                1020

cag  atg ctg aga acg ggc  aac aac ttt acc ttc  agc tac acc ttt      3470
Gln  Met Leu Arg Thr Gly  Asn Asn Phe Thr Phe  Ser Tyr Thr Phe
1025                1030                1035

gag  gaa gtg cct ttc cac  agc agc tac gcg cac  agc cag agc ctg      3515
Glu  Glu Val Pro Phe His  Ser Ser Tyr Ala His  Ser Gln Ser Leu
1040                1045                1050

gac  cgg ctg atg aat cct  ctc atc gac caa tac  ctg tat tac ctg      3560
Asp  Arg Leu Met Asn Pro  Leu Ile Asp Gln Tyr  Leu Tyr Tyr Leu
1055                1060                1065

aac  aga act caa aat cag  tcc gga agt gcc caa  aac aag gac ttg      3605
Asn  Arg Thr Gln Asn Gln  Ser Gly Ser Ala Gln  Asn Lys Asp Leu
1070                1075                1080

ctg  ttt agc cgt ggg tct  cca gct ggc atg tct  gtt cag ccc aaa      3650
Leu  Phe Ser Arg Gly Ser  Pro Ala Gly Met Ser  Val Gln Pro Lys
1085                1090                1095

aac  tgg cta cct gga ccc  tgt tat cgg cag cag  cgc gtt tct aaa      3695
Asn  Trp Leu Pro Gly Pro  Cys Tyr Arg Gln Gln  Arg Val Ser Lys
1100                1105                1110

aca  aaa aca gac aac aac  aac agc aat ttt acc  tgg act ggt gct      3740
Thr  Lys Thr Asp Asn Asn  Asn Ser Asn Phe Thr  Trp Thr Gly Ala
1115                1120                1125

tca  aaa tat aac ctc aat  ggg cgt gaa tcc atc  atc aac cct ggc      3785
Ser  Lys Tyr Asn Leu Asn  Gly Arg Glu Ser Ile  Ile Asn Pro Gly
1130                1135                1140

act  gct atg gcc tca cac  aaa gac gac gaa gac  aag ttc ttt ccc      3830
Thr  Ala Met Ala Ser His  Lys Asp Asp Glu Asp  Lys Phe Phe Pro
1145                1150                1155

atg  agc ggt gtc atg att  ttt gga aaa gag agc  gcc gga gct tca      3875
Met  Ser Gly Val Met Ile  Phe Gly Lys Glu Ser  Ala Gly Ala Ser
1160                1165                1170

aac  act gca ttg gac aat  gtc atg att aca gac  gaa gag gaa att      3920
Asn  Thr Ala Leu Asp Asn  Val Met Ile Thr Asp  Glu Glu Glu Ile
1175                1180                1185

aaa  gcc act aac cct gtg  gcc acc gaa aga ttt  ggg acc gtg gca      3965
Lys  Ala Thr Asn Pro Val  Ala Thr Glu Arg Phe  Gly Thr Val Ala
1190                1195                1200

gtc  aat ttc cag agc agc  agc aca gac cct gcg  acc gga gat gtg      4010
Val  Asn Phe Gln Ser Ser  Ser Thr Asp Pro Ala  Thr Gly Asp Val
1205                1210                1215
```

```
cat  gct atg gga gca tta  cct ggc atg gtg tgg  caa gat aga gac      4055
His  Ala Met Gly Ala Leu  Pro Gly Met Val Trp  Gln Asp Arg Asp
1220                 1225                 1230

gtg  tac ctg cag ggt ccc  att tgg gcc aaa att  cct cac aca gat      4100
Val  Tyr Leu Gln Gly Pro  Ile Trp Ala Lys Ile  Pro His Thr Asp
1235                 1240                 1245

gga  cac ttt cac ccg tct  cct ctt atg ggc ggc  ttt gga ctc aag      4145
Gly  His Phe His Pro Ser  Pro Leu Met Gly Gly  Phe Gly Leu Lys
1250                 1255                 1260

aac  ccg cct cct cag atc  ctc atc aaa aac acg  cct gtt cct gcg      4190
Asn  Pro Pro Pro Gln Ile  Leu Ile Lys Asn Thr  Pro Val Pro Ala
1265                 1270                 1275

aat  cct ccg gcg gag ttt  tca gct aca aag ttt  gct tca ttc atc      4235
Asn  Pro Pro Ala Glu Phe  Ser Ala Thr Lys Phe  Ala Ser Phe Ile
1280                 1285                 1290

acc  caa tac tcc aca gga  caa gtg agt gtg gaa  att gaa tgg gag      4280
Thr  Gln Tyr Ser Thr Gly  Gln Val Ser Val Glu  Ile Glu Trp Glu
1295                 1300                 1305

ctg  cag aaa gaa aac agc  aag cgc tgg aat ccc  gaa gtg cag tac      4325
Leu  Gln Lys Glu Asn Ser  Lys Arg Trp Asn Pro  Glu Val Gln Tyr
1310                 1315                 1320

aca  tcc aat tat gca aaa  tct gcc aac gtt gat  ttt act gtg gac      4370
Thr  Ser Asn Tyr Ala Lys  Ser Ala Asn Val Asp  Phe Thr Val Asp
1325                 1330                 1335

aac  aat gga ctt tat act  gag cct cgc ccc att  ggc acc cgt tac      4415
Asn  Asn Gly Leu Tyr Thr  Glu Pro Arg Pro Ile  Gly Thr Arg Tyr
1340                 1345                 1350

ctt  acc cgt ccc ctg taattacgtg ttaatcaata aaccggttga ttcgtttcag   4470
Leu  Thr Arg Pro Leu
1355

ttgaactttg gtctcctgtc cttcttatct tatcggttac catggttata gcttacacat   4530

taactgcttg gttgcgcttc gcgataaaag acttacgtca tcgggttacc cctagtgatg   4590

gagttgccca ctccctctct gcgcgctcgc tcgctcggtg gggcctgcgg accaaaggtc   4650

cgcagacggc agagctctgc tctgccggcc ccaccgagcg agcgagcgcg cagagaggga   4710

gtgggcaa                                                           4718
```

<210> 2
<211> 623
<212> PRT
<213> AAV-1

<400> 2

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15
```

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
20 25 30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
35 40 45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
50 55 60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65 70 75 80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
85 90 95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
100 105 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
115 120 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
130 135 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145 150 155 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
165 170 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
180 185 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
195 200 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
210 215 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225 230 235 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
275 280 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
565 570 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
580 585 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
595 600 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
610 615 620

<210> 3
<211> 736
<212> PRT
<213> AAV-1

<400> 3

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln

305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu

625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 4
<211> 1872
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1869)
<223>

<400> 4

```
atg ccg ggc ttc tac gag atc gtg atc aag gtg ccg agc gac ctg gac      48
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

gag cac ctg ccg ggc att tct gac tcg ttt gtg agc tgg gtg gcc gag      96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ctg ccc ccg gat tct gac atg gat ctg aat ctg att     144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttc ctg     192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

gtc caa tgg cgc cgc gtg agt aag gcc ccg gag gcc ctc ttc ttt gtt     240
Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

cag ttc gag aag ggc gag tcc tac ttc cac ctc cat att ctg gtg gag     288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

acc acg ggg gtc aaa tcc atg gtg ctg ggc cgc ttc ctg agt cag att     336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110
```

```
agg gac aag ctg gtg cag acc atc tac cgc ggg atc gag ccg acc ctg      384
Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

ccc aac tgg ttc gcg gtg acc aag acg cgt aat ggc gcc gga ggg ggg      432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

aac aag gtg gtg gac gag tgc tac atc ccc aac tac ctc ctg ccc aag      480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

act cag ccc gag ctg cag tgg gcg tgg act aac atg gag gag tat ata      528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

agc gcc tgt ttg aac ctg gcc gag cgc aaa cgg ctc gtg gcg cag cac      576
Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acc cac gtc agc cag acc cag gag cag aac aag gag aat ctg aac      624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

ccc aat tct gac gcg cct gtc atc cgg tca aaa acc tcc gcg cgc tac      672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag      720
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct      768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag      816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct      864
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg      912
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc      960
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc     1008
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc     1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350
```

```
ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat      1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc      1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc      1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg      1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc      1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt      1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag      1392
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg      1440
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc      1488
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc      1536
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc      1584
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

gac agg tac caa aac aaa tgt tct cgt cac gcg ggc atg ctt cag atg      1632
Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
    530                 535                 540

ctg ttt ccc tgc aag aca tgc gag aga atg aat cag aat ttc aac att      1680
Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545                 550                 555                 560

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg      1728
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt      1776
Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590
```

```
gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc     1824
Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ilé Ala Cys Ser Ala
        595                 600                 605

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa     1872
Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 5
<211> 623
<212> PRT
<213> AAV-1

<400> 5

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240
```

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
245 250 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
260 265 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
275 280 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
290 295 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305 310 315 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
325 330 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
340 345 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
355 360 365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
530 535 540

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
545 550 555 560

```
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
                565                 570                 575

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
            580                 585                 590

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
        595                 600                 605

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
    610                 615                 620
```

<210> 6
<211> 1641
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1638)
<223>

<400> 6

```
atg ccg ggc ttc tac gag atc gtg atc aag gtg ccg agc gac ctg gac        48
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                  10                  15

gag cac ctg ccg ggc att tct gac tcg ttt gtg agc tgg gtg gcc gag        96
Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

aag gaa tgg gag ctg ccc ccg gat tct gac atg gat ctg aat ctg att       144
Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45

gag cag gca ccc ctg acc gtg gcc gag aag ctg cag cgc gac ttc ctg       192
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

gtc caa tgg cgc cgc gtg agt aag gcc ccg gag gcc ctc ttc ttt gtt       240
Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

cag ttc gag aag ggc gag tcc tac ttc cac ctc cat att ctg gtg gag       288
Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

acc acg ggg gtc aaa tcc atg gtg ctg ggc cgc ttc ctg agt cag att       336
Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

agg gac aag ctg gtg cag acc atc tac cgc ggg atc gag ccg acc ctg       384
Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

ccc aac tgg ttc gcg gtg acc aag acg cgt aat ggc gcc gga ggg ggg       432
Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140
```

```
aac aag gtg gtg gac gag tgc tac atc ccc aac tac ctc ctg ccc aag      480
Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

act cag ccc gag ctg cag tgg gcg tgg act aac atg gag gag tat ata      528
Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

agc gcc tgt ttg aac ctg gcc gag cgc aaa cgg ctc gtg gcg cag cac      576
Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

ctg acc cac gtc agc cag acc cag gag cag aac aag gag aat ctg aac      624
Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

ccc aat tct gac gcg cct gtc atc cgg tca aaa acc tcc gcg cgc tac      672
Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag      720
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct      768
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag      816
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct      864
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg      912
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc      960
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc     1008
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc     1056
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat     1104
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc     1152
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370                 375                 380
```

```
aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc      1200
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385                 390                 395                 400

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg      1248
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
                405                 410                 415

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc      1296
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
            420                 425                 430

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt      1344
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
        435                 440                 445

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag      1392
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
    450                 455                 460

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg      1440
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465                 470                 475                 480

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc      1488
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
                485                 490                 495

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc      1536
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
            500                 505                 510

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc      1584
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
        515                 520                 525

gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa      1632
Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
    530                 535                 540

cct ctc tga                                                         1641
Pro Leu
545
```

<210> 7
<211> 546
<212> PRT
<213> AAV-1

<400> 7

```
Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val Pro Ser Asp Leu Asp
1               5                   10                  15

Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Ser Trp Val Ala Glu
            20                  25                  30

Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
        35                  40                  45
```

```
Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
    50                  55                  60

Val Gln Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65                  70                  75                  80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Leu His Ile Leu Val Glu
                85                  90                  95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100                 105                 110

Arg Asp Lys Leu Val Gln Thr Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115                 120                 125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130                 135                 140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145                 150                 155                 160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Glu Tyr Ile
                165                 170                 175

Ser Ala Cys Leu Asn Leu Ala Glu Arg Lys Arg Leu Val Ala Gln His
            180                 185                 190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Leu Asn
        195                 200                 205

Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
    210                 215                 220

Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
225                 230                 235                 240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
                245                 250                 255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
            260                 265                 270

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
        275                 280                 285

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
    290                 295                 300

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
305                 310                 315                 320

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
                325                 330                 335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
            340                 345                 350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355                 360                 365
```

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
370 375 380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385 390 395 400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
405 410 415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
420 425 430

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
435 440 445

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
450 455 460

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
465 470 475 480

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
485 490 495

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
500 505 510

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
515 520 525

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
530 535 540

Pro Leu
545

<210> 8
<211> 1200
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1197)
<223>

<400> 8
atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag 48
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1 5 10 15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct 96
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
20 25 30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag 144
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
35 40 45

```
atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct      192
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
    50                  55                  60

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg      240
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65                  70                  75                  80

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc      288
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc      336
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc      384
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat      432
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc      480
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc      528
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg      576
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc      624
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt      672
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag      720
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg      768
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
                245                 250                 255

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc      816
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
            260                 265                 270

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc      864
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285
```

```
gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc      912
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

gac agg tac caa aac aaa tgt tct cgt cac gcg ggc atg ctt cag atg      960
Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
305                 310                 315                 320

ctg ttt ccc tgc aag aca tgc gag aga atg aat cag aat ttc aac att     1008
Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
                325                 330                 335

tgc ttc acg cac ggg acg aga gac tgt tca gag tgc ttc ccc ggc gtg     1056
Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
            340                 345                 350

tca gaa tct caa ccg gtc gtc aga aag agg acg tat cgg aaa ctc tgt     1104
Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
        355                 360                 365

gcc att cat cat ctg ctg ggg cgg gct ccc gag att gct tgc tcg gcc     1152
Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
    370                 375                 380

tgc gat ctg gtc aac gtg gac ctg gat gac tgt gtt tct gag caa taa     1200
Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
385                 390                 395
```

<210> 9
<211> 399
<212> PRT
<213> AAV-1

<400> 9

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35                  40                  45

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
    50                  55                  60

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65                  70                  75                  80

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
```

130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
245 250 255

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
260 265 270

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
275 280 285

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
290 295 300

Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Ala Gly Met Leu Gln Met
305 310 315 320

Leu Phe Pro Cys Lys Thr Cys Glu Arg Met Asn Gln Asn Phe Asn Ile
325 330 335

Cys Phe Thr His Gly Thr Arg Asp Cys Ser Glu Cys Phe Pro Gly Val
340 345 350

Ser Glu Ser Gln Pro Val Val Arg Lys Arg Thr Tyr Arg Lys Leu Cys
355 360 365

Ala Ile His His Leu Leu Gly Arg Ala Pro Glu Ile Ala Cys Ser Ala
370 375 380

Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Val Ser Glu Gln
385 390 395

<210> 10
<211> 969
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(966)
<223>

<220>
<221> misc_feature
<222> (943)..(944)
<223> minor splice site

<400> 10

```
atg gag ctg gtc ggg tgg ctg gtg gac cgg ggc atc acc tcc gag aag        48
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                  10                  15

cag tgg atc cag gag gac cag gcc tcg tac atc tcc ttc aac gcc gct        96
Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

tcc aac tcg cgg tcc cag atc aag gcc gct ctg gac aat gcc ggc aag       144
Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35                  40                  45

atc atg gcg ctg acc aaa tcc gcg ccc gac tac ctg gta ggc ccc gct       192
Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
    50                  55                  60

ccg ccc gcg gac att aaa acc aac cgc atc tac cgc atc ctg gag ctg       240
Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65                  70                  75                  80

aac ggc tac gaa cct gcc tac gcc ggc tcc gtc ttt ctc ggc tgg gcc       288
Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95

cag aaa agg ttc ggg aag cgc aac acc atc tgg ctg ttt ggg ccg gcc       336
Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            100                 105                 110

acc acg ggc aag acc aac atc gcg gaa gcc atc gcc cac gcc gtg ccc       384
Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
        115                 120                 125

ttc tac ggc tgc gtc aac tgg acc aat gag aac ttt ccc ttc aat gat       432
Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
    130                 135                 140

tgc gtc gac aag atg gtg atc tgg tgg gag gag ggc aag atg acg gcc       480
Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145                 150                 155                 160

aag gtc gtg gag tcc gcc aag gcc att ctc ggc ggc agc aag gtg cgc       528
Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
                165                 170                 175

gtg gac caa aag tgc aag tcg tcc gcc cag atc gac ccc acc ccc gtg       576
Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            180                 185                 190

atc gtc acc tcc aac acc aac atg tgc gcc gtg att gac ggg aac agc       624
Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        195                 200                 205

acc acc ttc gag cac cag cag ccg ttg cag gac cgg atg ttc aaa ttt       672
```

```
Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
    210                 215                 220

gaa ctc acc cgc cgt ctg gag cat gac ttt ggc aag gtg aca aag cag      720
Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225                 230                 235                 240

gaa gtc aaa gag ttc ttc cgc tgg gcg cag gat cac gtg acc gag gtg      768
Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
                245                 250                 255

gcg cat gag ttc tac gtc aga aag ggt gga gcc aac aaa aga ccc gcc      816
Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
            260                 265                 270

ccc gat gac gcg gat aaa agc gag ccc aag cgg gcc tgc ccc tca gtc      864
Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
        275                 280                 285

gcg gat cca tcg acg tca gac gcg gaa gga gct ccg gtg gac ttt gcc      912
Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
    290                 295                 300

gac agg tat ggc tgc cga tgg tta tct tcc aga ttg gct cga gga caa      960
Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
305                 310                 315                 320

cct ctc tga                                                          969
Pro Leu
```

<210> 11
<211> 322
<212> PRT
<213> AAV-1

<220>
<221> misc_feature
<222> (943)..(944)
<223> minor splice site

<400> 11

```
Met Glu Leu Val Gly Trp Leu Val Asp Arg Gly Ile Thr Ser Glu Lys
1               5                   10                  15

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            20                  25                  30

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        35                  40                  45

Ile Met Ala Leu Thr Lys Ser Ala Pro Asp Tyr Leu Val Gly Pro Ala
    50                  55                  60

Pro Pro Ala Asp Ile Lys Thr Asn Arg Ile Tyr Arg Ile Leu Glu Leu
65                  70                  75                  80

Asn Gly Tyr Glu Pro Ala Tyr Ala Gly Ser Val Phe Leu Gly Trp Ala
                85                  90                  95
```

Gln Lys Arg Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
100 105 110

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Ala Val Pro
115 120 125

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
130 135 140

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
145 150 155 160

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
165 170 175

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
180 185 190

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
195 200 205

Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
210 215 220

Glu Leu Thr Arg Arg Leu Glu His Asp Phe Gly Lys Val Thr Lys Gln
225 230 235 240

Glu Val Lys Glu Phe Phe Arg Trp Ala Gln Asp His Val Thr Glu Val
245 250 255

Ala His Glu Phe Tyr Val Arg Lys Gly Gly Ala Asn Lys Arg Pro Ala
260 265 270

Pro Asp Asp Ala Asp Lys Ser Glu Pro Lys Arg Ala Cys Pro Ser Val
275 280 285

Ala Asp Pro Ser Thr Ser Asp Ala Glu Gly Ala Pro Val Asp Phe Ala
290 295 300

Asp Arg Tyr Gly Cys Arg Trp Leu Ser Ser Arg Leu Ala Arg Gly Gln
305 310 315 320

Pro Leu

<210> 12
<211> 2211
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(2208)
<223>

<400> 12
atg gct gcc gat ggt tat ctt cca gat tgg ctc gag gac aac ctc tct 48
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser

```
1                5                  10                  15

gag ggc att cgc gag tgg tgg gac ttg aaa cct gga gcc ccg aag ccc      96
Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

aaa gcc aac cag caa aag cag gac gac ggc cgg ggt ctg gtg ctt cct     144
Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

ggc tac aag tac ctc gga ccc ttc aac gga ctc gac aag ggg gag ccc     192
Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

gtc aac gcg gcg gac gca gcg gcc ctc gag cac gac aag gcc tac gac     240
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

cag cag ctc aaa gcg ggt gac aat ccg tac ctg cgg tat aac cac gcc     288
Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

gac gcc gag ttt cag gag cgt ctg caa gaa gat acg tct ttt ggg ggc     336
Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

aac ctc ggg cga gca gtc ttc cag gcc aag aag cgg gtt ctc gaa cct     384
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

ctc ggt ctg gtt gag gaa ggc gct aag acg gct cct gga aag aaa cgt     432
Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

ccg gta gag cag tcg cca caa gag cca gac tcc tcc tcg ggc atc ggc     480
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

aag aca ggc cag cag ccc gct aaa aag aga ctc aat ttt ggt cag act     528
Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

ggc gac tca gag tca gtc ccc gat cca caa cct ctc gga gaa cct cca     576
Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

gca acc ccc gct gct gtg gga cct act aca atg gct tca ggc ggt ggc     624
Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

gca cca atg gca gac aat aac gaa ggc gcc gac gga gtg ggt aat gcc     672
Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

tca gga aat tgg cat tgc gat tcc aca tgg ctg ggc gac aga gtc atc     720
Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

acc acc agc acc cgc acc tgg gcc ttg ccc acc tac aat aac cac ctc     768
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
```

```
                    245                 250                 255

tac aag caa atc tcc agt gct tca acg ggg gcc agc aac gac aac cac      816
Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

tac ttc ggc tac agc acc ccc tgg ggg tat ttt gat ttc aac aga ttc      864
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

cac tgc cac ttt tca cca cgt gac tgg cag cga ctc atc aac aac aat      912
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

tgg gga ttc cgg ccc aag aga ctc aac ttc aaa ctc ttc aac atc caa      960
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

gtc aag gag gtc acg acg aat gat ggc gtc aca acc atc gct aat aac     1008
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

ctt acc agc acg gtt caa gtc ttc tcg gac tcg gag tac cag ctt ccg     1056
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

tac gtc ctc ggc tct gcg cac cag ggc tgc ctc cct ccg ttc ccg gcg     1104
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

gac gtg ttc atg att ccg caa tac ggc tac ctg acg ctc aac aat ggc     1152
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

agc caa gcc gtg gga cgt tca tcc ttt tac tgc ctg gaa tat ttc cct     1200
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

tct cag atg ctg aga acg ggc aac aac ttt acc ttc agc tac acc ttt     1248
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

gag gaa gtg cct ttc cac agc agc tac gcg cac agc cag agc ctg gac     1296
Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

cgg ctg atg aat cct ctc atc gac caa tac ctg tat tac ctg aac aga     1344
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

act caa aat cag tcc gga agt gcc caa aac aag gac ttg ctg ttt agc     1392
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

cgt ggg tct cca gct ggc atg tct gtt cag ccc aaa aac tgg cta cct     1440
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

gga ccc tgt tat cgg cag cag cgc gtt tct aaa aca aaa aca gac aac     1488
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                    485                 490                 495

aac aac agc aat ttt acc tgg act ggt gct tca aaa tat aac ctc aat      1536
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

ggg cgt gaa tcc atc atc aac cct ggc act gct atg gcc tca cac aaa      1584
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

gac gac gaa gac aag ttc ttt ccc atg agc ggt gtc atg att ttt gga      1632
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

aaa gag agc gcc gga gct tca aac act gca ttg gac aat gtc atg att      1680
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

aca gac gaa gag gaa att aaa gcc act aac cct gtg gcc acc gaa aga      1728
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

ttt ggg acc gtg gca gtc aat ttc cag agc agc agc aca gac cct gcg      1776
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

acc gga gat gtg cat gct atg gga gca tta cct ggc atg gtg tgg caa      1824
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

gat aga gac gtg tac ctg cag ggt ccc att tgg gcc aaa att cct cac      1872
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

aca gat gga cac ttt cac ccg tct cct ctt atg ggc ggc ttt gga ctc      1920
Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

aag aac ccg cct cct cag atc ctc atc aaa aac acg cct gtt cct gcg      1968
Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

aat cct ccg gcg gag ttt tca gct aca aag ttt gct tca ttc atc acc      2016
Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

caa tac tcc aca gga caa gtg agt gtg gaa att gaa tgg gag ctg cag      2064
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

aaa gaa aac agc aag cgc tgg aat ccc gaa gtg cag tac aca tcc aat      2112
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

tat gca aaa tct gcc aac gtt gat ttt act gtg gac aac aat gga ctt      2160
Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

tat act gag cct cgc ccc att ggc acc cgt tac ctt acc cgt ccc ctg      2208
Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
```

725 730 735

taa 2211

<210> 13
<211> 736
<212> PRT
<213> AAV-1

<400> 13

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His

260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala

580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 14
<211> 1800
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1797)
<223>

<400> 14
acg gct cct gga aag aaa cgt ccg gta gag cag tcg cca caa gag cca 48
Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro
1 5 10 15

gac tcc tcc tcg ggc atc ggc aag aca ggc cag cag ccc gct aaa aag 96
Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys
20 25 30

aga ctc aat ttt ggt cag act ggc gac tca gag tca gtc ccc gat cca 144
Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro
35 40 45

caa cct ctc gga gaa cct cca gca acc ccc gct gct gtg gga cct act 192
Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr
50 55 60

aca atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc 240
Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
65 70 75 80

```
gcc gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca      288
Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr
                85                  90                  95

tgg ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg      336
Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
            100                 105                 110

ccc acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg      384
Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr
        115                 120                 125

ggg gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg      432
Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
    130                 135                 140

tat ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg      480
Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
145                 150                 155                 160

cag cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac      528
Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
                165                 170                 175

ttc aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc      576
Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly
            180                 185                 190

gtc aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg      624
Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser
        195                 200                 205

gac tcg gag tac cag ctt ccg tac gtc ctc ggc tct gcg cac cag ggc      672
Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
    210                 215                 220

tgc ctc cct ccg ttc ccg gcg gac gtg ttc atg att ccg caa tac ggc      720
Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
225                 230                 235                 240

tac ctg acg ctc aac aat ggc agc caa gcc gtg gga cgt tca tcc ttt      768
Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
                245                 250                 255

tac tgc ctg gaa tat ttc cct tct cag atg ctg aga acg ggc aac aac      816
Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
            260                 265                 270

ttt acc ttc agc tac acc ttt gag gaa gtg cct ttc cac agc agc tac      864
Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr
        275                 280                 285

gcg cac agc cag agc ctg gac cgg ctg atg aat cct ctc atc gac caa      912
Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
    290                 295                 300

tac ctg tat tac ctg aac aga act caa aat cag tcc gga agt gcc caa      960
Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln
305                 310                 315                 320
```

```
gaa gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt      1728
Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe
                565                 570                 575

act gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc      1776
Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr
            580                 585                 590

cgt tac ctt acc cgt ccc ctg taa                                     1800
Arg Tyr Leu Thr Arg Pro Leu
        595
```

<210> 15
<211> 599
<212> PRT
<213> AAV-1

<400> 15

```
Thr Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro Gln Glu Pro
1               5                  10                  15

Asp Ser Ser Ser Gly Ile Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys
            20                  25                  30

Arg Leu Asn Phe Gly Gln Thr Gly Asp Ser Glu Ser Val Pro Asp Pro
        35                  40                  45

Gln Pro Leu Gly Glu Pro Pro Ala Thr Pro Ala Ala Val Gly Pro Thr
    50                  55                  60

Thr Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly
65                  70                  75                  80

Ala Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr
                85                  90                  95

Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu
            100                 105                 110

Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr
        115                 120                 125

Gly Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly
    130                 135                 140

Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp
145                 150                 155                 160

Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn
                165                 170                 175

Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly
            180                 185                 190

Val Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser
        195                 200                 205

Asp Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly
```

```
    210                 215                 220
Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly
225                 230                 235                 240
Tyr Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe
                245                 250                 255
Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn
            260                 265                 270
Phe Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr
        275                 280                 285
Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln
    290                 295                 300
Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln
305                 310                 315                 320
Asn Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val
                325                 330                 335
Gln Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val
            340                 345                 350
Ser Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly
        355                 360                 365
Ala Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly
    370                 375                 380
Thr Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met
385                 390                 395                 400
Ser Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr
                405                 410                 415
Ala Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr
            420                 425                 430
Asn Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln
        435                 440                 445
Ser Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala
    450                 455                 460
Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
465                 470                 475                 480
Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro
                485                 490                 495
Leu Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile
            500                 505                 510
Lys Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr
        515                 520                 525
Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
```

530 535 540

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
545 550 555 560

Glu Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe
565 570 575

Thr Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr
580 585 590

Arg Tyr Leu Thr Arg Pro Leu
595

<210> 16
<211> 1605
<212> DNA
<213> AAV-1

<220>
<221> CDS
<222> (1)..(1602)
<223>

<400> 16

atg gct tca ggc ggt ggc gca cca atg gca gac aat aac gaa ggc gcc 48
Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
1 5 10 15

gac gga gtg ggt aat gcc tca gga aat tgg cat tgc gat tcc aca tgg 96
Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp
20 25 30

ctg ggc gac aga gtc atc acc acc agc acc cgc acc tgg gcc ttg ccc 144
Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
35 40 45

acc tac aat aac cac ctc tac aag caa atc tcc agt gct tca acg ggg 192
Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly
50 55 60

gcc agc aac gac aac cac tac ttc ggc tac agc acc ccc tgg ggg tat 240
Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65 70 75 80

ttt gat ttc aac aga ttc cac tgc cac ttt tca cca cgt gac tgg cag 288
Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
85 90 95

cga ctc atc aac aac aat tgg gga ttc cgg ccc aag aga ctc aac ttc 336
Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe
100 105 110

aaa ctc ttc aac atc caa gtc aag gag gtc acg acg aat gat ggc gtc 384
Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val
115 120 125

aca acc atc gct aat aac ctt acc agc acg gtt caa gtc ttc tcg gac 432
Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp

```
    130                 135                 140

tcg gag tac cag ctt ccg tac gtc ctc ggc tct gcg cac cag ggc tgc      480
Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys
145                 150                 155                 160

ctc cct ccg ttc ccg gcg gac gtg ttc atg att ccg caa tac ggc tac      528
Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr
                165                 170                 175

ctg acg ctc aac aat ggc agc caa gcc gtg gga cgt tca tcc ttt tac      576
Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr
            180                 185                 190

tgc ctg gaa tat ttc cct tct cag atg ctg aga acg ggc aac aac ttt      624
Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
        195                 200                 205

acc ttc agc tac acc ttt gag gaa gtg cct ttc cac agc agc tac gcg      672
Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala
    210                 215                 220

cac agc cag agc ctg gac cgg ctg atg aat cct ctc atc gac caa tac      720
His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
225                 230                 235                 240

ctg tat tac ctg aac aga act caa aat cag tcc gga agt gcc caa aac      768
Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn
                245                 250                 255

aag gac ttg ctg ttt agc cgt ggg tct cca gct ggc atg tct gtt cag      816
Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln
            260                 265                 270

ccc aaa aac tgg cta cct gga ccc tgt tat cgg cag cag cgc gtt tct      864
Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
        275                 280                 285

aaa aca aaa aca gac aac aac aac agc aat ttt acc tgg act ggt gct      912
Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala
    290                 295                 300

tca aaa tat aac ctc aat ggg cgt gaa tcc atc atc aac cct ggc act      960
Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr
305                 310                 315                 320

gct atg gcc tca cac aaa gac gac gaa gac aag ttc ttt ccc atg agc     1008
Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser
                325                 330                 335

ggt gtc atg att ttt gga aaa gag agc gcc gga gct tca aac act gca     1056
Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala
            340                 345                 350

ttg gac aat gtc atg att aca gac gaa gag gaa att aaa gcc act aac     1104
Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
        355                 360                 365

cct gtg gcc acc gaa aga ttt ggg acc gtg gca gtc aat ttc cag agc     1152
Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser
```

```
    370                 375                 380
agc agc aca gac cct gcg acc gga gat gtg cat gct atg gga gca tta      1200
Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu
385                 390                 395                 400

cct ggc atg gtg tgg caa gat aga gac gtg tac ctg cag ggt ccc att      1248
Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
                405                 410                 415

tgg gcc aaa att cct cac aca gat gga cac ttt cac ccg tct cct ctt      1296
Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
            420                 425                 430

atg ggc ggc ttt gga ctc aag aac ccg cct cct cag atc ctc atc aaa      1344
Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys
        435                 440                 445

aac acg cct gtt cct gcg aat cct ccg gcg gag ttt tca gct aca aag      1392
Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys
    450                 455                 460

ttt gct tca ttc atc acc caa tac tcc aca gga caa gtg agt gtg gaa      1440
Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
465                 470                 475                 480

att gaa tgg gag ctg cag aaa gaa aac agc aag cgc tgg aat ccc gaa      1488
Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
                485                 490                 495

gtg cag tac aca tcc aat tat gca aaa tct gcc aac gtt gat ttt act      1536
Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr
            500                 505                 510

gtg gac aac aat gga ctt tat act gag cct cgc ccc att ggc acc cgt      1584
Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
        515                 520                 525

tac ctt acc cgt ccc ctg taa                                         1605
Tyr Leu Thr Arg Pro Leu
    530
```

<210> 17
<211> 534
<212> PRT
<213> AAV-1

<400> 17

```
Met Ala Ser Gly Gly Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala
1               5                   10                  15

Asp Gly Val Gly Asn Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp
            20                  25                  30

Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro
        35                  40                  45

Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly
    50                  55                  60
```

Ala Ser Asn Asp Asn His Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
65 70 75 80

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
85 90 95

Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe
100 105 110

Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val
115 120 125

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Ser Asp
130 135 140

Ser Glu Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys
145 150 155 160

Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr
165 170 175

Leu Thr Leu Asn Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr
180 185 190

Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe
195 200 205

Thr Phe Ser Tyr Thr Phe Glu Glu Val Pro Phe His Ser Ser Tyr Ala
210 215 220

His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr
225 230 235 240

Leu Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn
245 250 255

Lys Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln
260 265 270

Pro Lys Asn Trp Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser
275 280 285

Lys Thr Lys Thr Asp Asn Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala
290 295 300

Ser Lys Tyr Asn Leu Asn Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr
305 310 315 320

Ala Met Ala Ser His Lys Asp Asp Glu Asp Lys Phe Phe Pro Met Ser
325 330 335

Gly Val Met Ile Phe Gly Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala
340 345 350

Leu Asp Asn Val Met Ile Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn
355 360 365

Pro Val Ala Thr Glu Arg Phe Gly Thr Val Ala Val Asn Phe Gln Ser
370 375 380

Ser Ser Thr Asp Pro Ala Thr Gly Asp Val His Ala Met Gly Ala Leu
385 390 395 400

Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile
405 410 415

Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
420 425 430

Met Gly Gly Phe Gly Leu Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys
435 440 445

Asn Thr Pro Val Pro Ala Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys
450 455 460

Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu
465 470 475 480

Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
485 490 495

Val Gln Tyr Thr Ser Asn Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr
500 505 510

Val Asp Asn Asn Gly Leu Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg
515 520 525

Tyr Leu Thr Arg Pro Leu
530

<210> 18
<211> 4681
<212> DNA
<213> AAV-2

<400> 18
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagccgcc atgccggggt tttacgagat tgtgattaag gtccccagcg 360

accttgacgg gcatctgccc ggcatttctg acagctttgt gaactgggtg gccgagaagg 420

aatgggagtt gccgccagat tctgacatgg atctgaatct gattgagcag gcacccctga 480

ccgtggccga gaagctgcag cgcgactttc tgacggaatg gcgccgtgtg agtaaggccc 540

cggaggccct tttctttgtg caatttgaga agggagagag ctacttccac atgcacgtgc 600

tcgtggaaac caccggggtg aaatccatgg ttttgggacg tttcctgagt cagattcgcg 660

aaaaactgat tcagagaatt taccgcggga tcgagccgac tttgccaaac tggttcgcgg 720

tcacaaagac cagaaatggc gccggaggcg ggaacaaggt ggtggatgag tgctacatcc 780

ccaattactt gctccccaaa acccagcctg agctccagtg ggcgtggact aatatggaac 840

agtatttaag cgcctgtttg aatctcacgg agcgtaaacg gttggtggcg cagcatctga 900

cgcacgtgtc gcagacgcag gagcagaaca aagagaatca gaatcccaat tctgatgcgc 960

cggtgatcag atcaaaaact tcagccaggt acatggagct ggtcgggtgg ctcgtggaca 1020

aggggattac ctcggagaag cagtggatcc aggaggacca ggcctcatac atctccttca 1080

atgcggcctc caactcgcgg tcccaaatca aggctgcctt ggacaatgcg ggaaagatta 1140

tgagcctgac taaaaccgcc cccgactacc tggtgggcca gcagcccgtg gaggacattt 1200

ccagcaatcg gatttataaa attttggaac taaacgggta cgatccccaa tatgcggctt 1260

ccgtctttct gggatgggcc acgaaaaagt tcggcaagag gaacaccatc tggctgtttg 1320

ggcctgcaac taccgggaag accaacatcg cggaggccat agcccacact gtgcccttct 1380

acgggtgcgt aaactggacc aatgagaact ttcccttcaa cgactgtgtc gacaagatgg 1440

tgatctggtg ggaggagggg aagatgaccg ccaaggtcgt ggagtcggcc aaagccattc 1500

tcggaggaag caaggtgcgc gtggaccaga aatgcaagtc ctcggcccag atagacccga 1560

ctcccgtgat cgtcacctcc aacaccaaca tgtgcgccgt gattgacggg aactcaacga 1620

ccttcgaaca ccagcagccg ttgcaagacc ggatgttcaa atttgaactc acccgccgtc 1680

tggatcatga ctttgggaag gtcaccaagc aggaagtcaa agacttttc cggtgggcaa 1740

aggatcacgt ggttgaggtg gagcatgaat tctacgtcaa aaagggtgga gccaagaaaa 1800

gacccgcccc cagtgacgca gatataagtg agcccaaacg ggtgcgcgag tcagttgcgc 1860

agccatcgac gtcagacgcg gaagcttcga tcaactacgc agacaggtac caaaacaaat 1920

gttctcgtca cgtgggcatg aatctgatgc tgtttccctg cagacaatgc gagagaatga 1980

atcagaattc aaatatctgc ttcactcacg gacagaaaga ctgtttagag tgctttcccg 2040

tgtcagaatc tcaaccggtt tctgtcgtca aaaaggcgta tcagaaactg tgctacattc 2100

atcatatcat gggaaaggtg ccagacgctt gcactgcctg cgatctggtc aatgtggatt 2160

tggatgactg catctttgaa caataaatga tttaaatcag gtatggctgc cgatggttat 2220

cttccagatt ggctcgagga cactctctct gaaggaataa gacagtggtg gaagctcaaa 2280

cctggcccac caccaccaaa gcccgcagag cggcataagg acgacagcag gggtcttgtg 2340

cttcctgggt acaagtacct cggacccttc aacggactcg acaagggaga gccggtcaac 2400

gaggcagacg ccgcggccct cgagcacgac aaagcctacg accggcagct cgacagcgga 2460

gacaacccgt acctcaagta caaccacgcc gacgcggagt ttcaggagcg ccttaaagaa 2520

gatacgtctt ttgggggcaa cctcggacga gcagtcttcc aggcgaaaaa gagggttctt 2580

gaacctctcg gcctggttga ggaacctgtt aagacggctc cgggaaaaaa gaggccggta 2640

gagcactctc ctgtggagcc agactcctcc tcgggaaccg gaaagccggg ccagcagcct 2700

gcaagaaaaa gattgaattt tggtcagact ggagacgcag actcagtacc tgacccccag 2760

cctctcggac agccaccagc agccccctct ggtctgggaa ctaatacgat ggctacaggc 2820

agtggcgcac caatggcaga caataacgag ggcgccgacg gagtgggtaa ttcctccgga 2880

aattggcatt gcgattccac atggatgggc gacagagtca tcaccaccag cacccgaacc 2940

tgggccctgc ccacctacaa caaccacctc tacaaacaaa tttccagcca atcaggagcc 3000

tcgaacgaca atcactactt tggctacagc acccccttggg ggtattttga cttcaacaga 3060

ttccactgcc acttttcacc acgtgactgg caaagactca tcaacaacaa ctggggattc 3120

cgacccaaga gactcaactt caacctcttt aacattcaag tcaaagaggt cacgcagaat 3180

gacggtacga cgacgattgc caataacctt accagcacgg ttcaggtgtt tactgactcg 3240

gagtaccagc tcccgtacgt cctcggctcg gcgcatcaag gatgcctccc gccgttccca 3300

gcagacgtct tcatggtgcc acagtatgga tacctcaccc tgaacaacgg gagtcaggca 3360

gtaggacgct cttcatttta ctgcctggag tactttcctt ctcagatgct gcgtaccgga 3420

aacaacttta ccttcagcta cacttttgag gacgttcctt tccacagcag ctacgctcac 3480

agccagagtc tggaccgtct catgaatcct ctcatcgacc agtacctgta ttacttgagc 3540

agaacaaaca ctccaagtgg aaccaccacg cagtcaaggc ttcagttttc tcaggcccca 3600

gccagtgaca ttcgggacca gtctaggaac tggcttcctg gaccctgtta ccgccagcag 3660

cgagtatgaa agacatctgc ggataacaac aacagtgaat actcgtggac tggagctacc 3720

aagtaccacc tcaatggcag agactctctg gtgaatccgg ggcccgccat ggcaagccac 3780

aaggacgatg aagaaaagtt ttttcctcag agcggggttc tcatctttgg gaagcaaggc 3840

tcagagaaaa caaatgtgaa cattgaaaag gtcatgatta cagacgaaga ggaaatccca 3900

acaaccaatc ccgtggctac ggagcagtat ggttctgtat ctaccaacct ccagagaggc 3960

aacagacaag cagctaccgc agatgtcaac acacaaggcg ttcttccagg catggtctgg 4020

caggacagag atgtgtacct tcaggggccc atctgggcaa agattccaca cacggacgga 4080

cattttcacc cctctcccct catgggtgga ttcggactta aacaccctcc tccacagatt 4140

ctcatcaaga acaccccggt acctgcgaat ccttcgacca ccttcagtgc ggcaaagttt 4200

gcttccttca tcacacagta ctccacggga cacggtcagc gtggagatcg agtgggagct 4260

gcagaacgaa aacagcaaac gctggaatcc cgaaattcag tacacttcca actacaacaa 4320

gtctgttaat cgtggacttt accgtggata ctaatggcgt gtattcagag cctcgcccca 4380

ttggcaccag atacctgact cgtaatctgt aattgcttgt taatcaataa accgtttaat 4440

tcgtttcagt tgaactttgg tctctgcgta tttctttctt atctagtttc catggctacg 4500

tagataagta gcatggcggg ttaatcatta actacaagga acccctagtg atggagttgg 4560

ccactccctc tctgcgcgct cgctcgctca ctgaggccgg gcgaccaaag gtcgcccgac 4620

gcccgggctt tgccccggcg gcctcagtga gcgagcgagc gcgcagagag ggagtgggca 4680

a 4681

<210> 19
<211> 4683
<212> DNA
<213> AAV-6

<400> 19
ttggccactc cctctctgcg cgctcgctcg ctcactgagg ccgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120

gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag 180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat 240

gtggtcacgc tgggtattta agcccgagtg agcacgcagg gtctccattt tgaagcggga 300

ggtttgaacg cgcagcgcca tgccggggtt ttacgagatt gtgattaagg tccccagcga 360

ccttgacgag catctgcccg gcatttctga cagctttgtg aactgggtgg ccgagaagga 420

atgggagttg ccgccagatt ctgacatgga tctgaatctg attgagcagg cacccctgac 480

cgtggccgag aagctgcagc gcgacttcct ggtccactgg cgccgcgtga gtaaggcccc 540

ggaggccctc ttctttgttc agttcgagaa gggcgagtcc tacttccacc tccatattct 600

ggtggagacc acgggggtca aatccatggt gctgggccgc ttcctgagtc agattagcga 660

caagctggtg cagaccatct accgcgggat cgagccgacc ctgcccaact ggttcgcggt 720

gaccaagacg cgtaatggcg ccggaggggg gaacaaggtg gtggacgagt gctacatccc 780

caactacctc ctgcccaaga ctcagcccga gctgcagtgg gcgtggacta acatggagga 840

gtatataagc gcgtgtttaa acctggccga gcgcaaacgg ctcgtggcgc acgacctgac 900

ccacgtcagc cagacccagg agcagaacaa ggagaatctg aaccccaatt ctgacgcgcc 960

tgtcatccgg tcaaaaacct ccgcacgcta catggagctg gtcgggtggc tggtggaccg 1020

gggcatcacc tccgagaagc agtggatcca ggaggaccag gcctcgtaca tctccttcaa 1080

cgccgcctcc aactcgcggt cccagatcaa ggccgctctg gacaatgccg gcaagatcat 1140

ggcgctgacc aaatccgcgc ccgactacct ggtaggcccc gctccgcccg ccgacattaa 1200

aaccaaccgc atttaccgca tcctggagct gaacggctac gaccctgcct acgccggctc 1260

cgtctttctc ggctgggccc agaaaaggtt cggaaaacgc aacaccatct ggctgtttgg 1320

gccggccacc acgggcaaga ccaacatcgc ggaagccatc gcccacgccg tgcccttcta 1380

cggctgcgtc aactggacca atgagaactt tcccttcaac gattgcgtcg acaagatggt 1440

gatctggtgg gaggagggca agatgacggc caaggtcgtg gagtccgcca aggccattct 1500

cggcggcagc aaggtgcgcg tggaccaaaa gtgcaagtcg tccgcccaga tcgatcccac 1560

ccccgtgatc gtcacctcca acaccaacat gtgcgccgtg attgacggga acagcaccac 1620

cttcgagcac cagcagccgt tgcaggaccg gatgttcaaa tttgaactca cccgccgtct 1680

ggagcatgac tttggcaagg tgacaaagca ggaagtcaaa gagttcttcc gctgggcgca 1740

ggatcacgtg accgaggtgg cgcatgagtt ctacgtcaga aagggtggag ccaacaacag 1800

acccgccccc gatgacgcgg ataaaagcga gcccaagcgg gcctgccccc cagtcgcgga 1860

tccatcgacg tcagacgcgg aaggagctcc ggtggacttt gccgacaggt accaaaacaa 1920

atgttctcgt cacgcgggca tgcttcagat gctgtttccc tgcaaaacat gcgagagaat 1980

gaatcagaat ttcaacattt gcttcacgca cgggaccaga gactgttcag aatgtttccc 2040

cggcgtgtca gaatctcaac cggtcgtcag aaagaggacg tatcggaaac tctgtgccat 2100

tcatcatctg ctggggcggg ctcccgagat tgcttgctcg gcctgcgatc tggtcaacgt 2160

ggatctggat gactgtgttt ctgagcaata aatgacttaa accaggtatg gctgccgatg 2220

gttatcttcc agattggctc gaggacaacc tctctgaggg cattcggcag tggtgggact 2280

tgaaacctgg agccccgaaa cccaaagcca accagcaaaa gcaggacgac ggccggggtc 2340

tggtgcttcc tggctacaag tacctcggac ccttcaacgg actcgacaag ggggagcccg 2400

tcaacgcggc ggatgcagcg gccctcgagc acgacaaggc ctacgaccag cagctcaaag 2460

cgggtgacaa tccgtacctg cggtataacc acgccgacgc cgagtttcag gagcgtctgc 2520

aagaagatac gtcttttggg ggcaacctcg ggcgagcagt cttccaggcc aagaagaggg 2580

ttctcgaacc ttttggtctg gttgaggaag gtgctaagac ggctcctgga aagaaacgtc 2640

cggtagagca gtcgccacaa gagccagact cctcctcggg cattggcaag acaggccagc 2700

agcccgctaa aaagagactc aattttggtc agactggcga ctcagagtca gtccccgacc 2760

cacaacctct cggagaacct ccagcaaccc ccgctgctgt gggacctact acaatggctt 2820

caggcggtgg cgcaccaatg gcagacaata acgaaggcgc cgacggagtg ggtaatgcct 2880

caggaaattg gcattgcgat tccacatggc tgggcgacag agtcatcacc accagcaccc 2940

gaacatgggc cttgcccacc tataacaacc acctctacaa gcaaatctcc agtgcttcaa 3000

cgggggccag caacgacaac cactacttcg gctacagcac cccctggggg tattttgatt 3060

tcaacagatt ccactgccat ttctcaccac gtgactggca gcgactcatc aacaacaatt 3120

ggggattccg gcccaagaga ctcaacttca agctcttcaa catccaagtc aaggaggtca 3180

cgacgaatga tggcgtcacg accatcgcta ataaccttac cagcacggtt caagtcttgt 3240

cggactcgga gtaccagttc ccgtacgtcc tcggctctgc gcaccagggc tgcctccctc 3300

cgttcccggc ggacgtgttc atgattccgc agtacggcta cctaacgctc aacaatggca 3360

gccaggcagt gggacgctca tccttttact gcctggaata tttcccatcg cagatgctga 3420

gaacgggcaa taactttacc ttcagctaca ccttcgagga cgtgcctttc cacagcagct 3480

acgcgcacag ccagagcctg gaccggctga tgaatcctct catcgaccag tacctgtatt 3540

acctgaacag aactcacaat cagtccggaa gtgcccaaaa caaggacttg ctgtttagcc 3600

gtgggtctcc agctggcatg tctgttcagc ccaaaaactg gctacctgga ccctgttacc 3660

ggcagcagcg cgtttctaaa acaaaaacag acaacaacaa cagcaacttt acctggactg 3720

gtgcttcaaa atataacctt aatgggcgtg aatctataat caaccctggc actgctatgg 3780

cctcacacaa agacgacaaa gacaagttct ttcccatgag cggtgtcatg atttttggaa 3840

aggagagcgc cggagcttca aacactgcat tggacaatgt catgatcaca gacgaagagg 3900

aaatcaaagc cactaacccc gtggccaccg aaagatttgg gactgtggca gtcaatctcc 3960

agagcagcag cacagaccct gcgaccggag atgtgcatgt tatgggagcc ttacctggaa 4020

tggtgtggca agacagagac gtatacctgc agggtcctat ttgggccaaa attcctcaca 4080

cggatggaca ctttcacccg tctcctctca tgggcggctt tggacttaag cacccgcctc 4140

ctcagatcct catcaaaaac acgcctgttc ctgcgaatcc tccggcagag ttttcggcta 4200

caaagtttgc ttcattcatc acccagtatt ccacaggaca agtgagcgtg gagattgaat 4260

gggagctgca gaaagaaaac agcaaacgct ggaatcccga agtgcagtat acatctaact 4320

atgcaaaatc tgccaacgtt gatttcactg tggacaacaa tggactttat actgagcctc 4380

gccccattgg cacccgttac ctcacccgtc ccctgtaatt gtgtgttaat caataaaccg 4440

gttaattcgt gtcagttgaa ctttggtctc atgtccttat tatcttatct ggtcaccata 4500

gcaaccggtt acacattaac tgcttagttg cgcttcgcga atacccctag tgatggagtt 4560

gcccactccc tctatgcgcg ctcgctcgct cggtggggcc ggcagagcag agctctgccg 4620

tctgcggacc tttggtccgc aggccccacc gagcgagcga gcgcgcatag agggagtggc 4680

caa 4683

<210> 20
<211> 16
<212> DNA
<213> rep binding motif

<400> 20
gctcgctcgc tcgctg 16